



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 122411

TO: Karen A Lacourciere
Location: REM-2D15/2C18
Art Unit: 1635
May 24, 2004

Case Serial Number: 09/301380

From: P. Sheppard
Location: Remsen Building
Phone: (571) 272-2529

sheppard@uspto.gov

Search Notes

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 22, 2004, 20:13:21 ; Search time 1486 Seconds
(without alignments)
11818.338 Million cell updates/sec

Title: US-09-301-380-1
Perfect score: 4134
Sequence: 1 ctcaagaatccccgcacga.....tggtagagagatattttc 4134

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_29Jan04:*
1: geneseqn19808:*
2: geneseqn19908:*
3: geneseqn20008:*
4: geneseqn20018:*
5: geneseqn20018:*
6: geneseqn20028:*
7: geneseqn20038:*
8: geneseqn20038:*
9: geneseqn20038:*
10: geneseqn20048:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4134	100.0	4134	3	AAZ38152 Human Nr-
2	3751.6	90.7	3997	2	AAV62739 Human neu
3	3316	80.2	6253	3	AAV64155 Nucleotid
4	3316	80.2	6254	2	AAV40887 Coding se
5	3316	80.2	6254	5	AAFP8452 Human CDN
6	3233.6	78.2	6384	10	ADE77114 Human CDN
7	2226	54.1	3943	6	AA516294 CDNA enco
8	1371	33.2	1371	3	AAZ38181 Human Nr-
9	1092.6	26.4	1371	3	AAZ38182 Rat Nr-CA
10	779.8	18.9	4360	7	AAAD9596 Human cyt
11	778.2	18.8	4080	7	AAAD9595 Human cyt
12	737.2	17.8	4131	7	ABR16046 NOVX rela
13	702.4	17.0	4739	4	AAKS1848 Human pol
14	676.6	16.4	4694	4	AAKS1847 Human pol
15	445.4	10.8	2462	9	ADBE1924 Human CDN
16	405.8	9.8	3783	6	AA516288 CDNA enco
17	405.4	9.8	5093	9	ADBS2876 Primary r
18	379	9.2	7722	5	AA585546 DNA enco
19	358.6	8.7	416	2	AAV87228 EST clone
20	351	8.5	3774	2	AAAO1588 Human LI
21	347	8.4	3888	6	AA516282 CDNA enco
22	340	8.2	445	4	ABAS7607 Human foe
23	340	8.2	445	4	AA137168 Probe #58

C 24	340	8.2	445	4	AAK31269 Human bon
C 25	340	8.2	445	4	AAK05659 Human bra
C 26	340	8.2	445	4	ABS30949 Human liv
C 27	340	8.2	445	6	ABS06021 Human gen
C 28	340	8.2	3250	4	AA105627 Human rep
C 29	284.4	6.9	694	6	ABT09020 Phase-1 R
C 30	231.8	5.6	32176	4	AA105628 Human rep
C 31	231	5.6	469	4	ABA58940 Human foe
C 32	231	5.6	469	4	AA138658 Probe #73
C 33	231	5.6	469	4	AAK32843 Human bon
C 34	231	5.6	469	4	AAK07103 Human bra
C 35	231	5.6	469	4	ABS32568 Human liv
C 36	231	5.6	469	6	ABS07647 Human gen
C 37	230	5.6	230	4	ABA70229 Human foe
C 38	230	5.6	230	4	AA150358 Probe #19
C 39	230	5.6	230	4	AAK44359 Human bon
C 40	230	5.6	230	4	AAK18454 Human bra
C 41	230	5.6	230	4	ABS44016 Human liv
C 42	230	5.6	230	6	ABS18595 Human gen
C 43	224	5.4	224	4	ABA71469 Human foe
C 44	224	5.4	224	4	AA151738 Probe #20
C 45	224	5.4	224	4	AAK45811 Human bon

ALIGNMENTS

RESULT 1	AAZ38152 standard; DNA; 4134 BP.
ID	AAZ38152
AC	AAZ38152;
XX	
DT	14-FEB-2000 (first entry)
XX	
DE	Human Nr-CAM gene sequence.
XX	
KW	Nr-CAM; neuron-glia-related cell adhesion molecule; cell proliferation;
KW	tumorigenesis; malignancy; cancer; leukemia; hyperproliferative disorder;
KW	degenerative disorder; growth deficiency; trauma; wound; tumor; diabetes;
KW	systemic lupus erythematosus; demyelinating disease; growth; ss.
XX	
OS	Homo sapiens.
XX	
PN	MO9955380-A1.
XX	
PD	04-NOV-1999.
XX	
PF	27-APR-1999; 99WO-US009039.
XX	
PR	27-APR-1998; 98US-0083152P.
PR	14-DEC-1998; 98US-0112098P.
XX	
PA	(PACI-) PACIFIC NORTHWEST CANCER FOUND.
PI	Murphy GP, Boynton AL, Sehgal A;
XX	
XX	WPI, 2000-023268/02.
DR	P-PSDB; AAY40439.
XX	
PT	Use of neuron-glia-related cell adhesion molecule for developing agents
PT	for the diagnosis and treatment of e.g. cancers, hyperproliferative
PT	disorders, growth deficiencies, degenerative disorders, trauma or wounds.
XX	
PS	Disclosure; Page 165-171; 183pp; English.
XX	
CC	The invention relates to the use of neuron-glia-related cell adhesion
CC	molecule (Nr-CAM) as a marker for diagnosing, treating, inhibiting or
CC	preventing disorders involving cell proliferation. An antisense nucleic
CC	acid complementary to at least a portion of an RNA transcript of a Nr-CAM
CC	gene can be used to inhibit hyperproliferation of a tumor cell, for the
CC	treatment of tumorigenesis. Agents which inhibit Nr-CAM function can be
CC	used to treat or prevent malignancies, e.g. brain cancer, leukemia, B

cell lymphoma, premalignant conditions, benign tumors, hyperproliferative
disorders or benign dysproliferative disorders. Such treatment is
especially useful for treating glioblastoma, glioma, meningioma,
astrocytoma, medulloblastoma, neuroectodermal cancer and neuroblastoma,
especially glioblastoma multiforme. Agents which promote Nr-CAM function
may also be used to treat or prevent degenerative disorders, growth
deficiencies, hypoproliferative disorders, physical trauma, lesions or
wounds. In particular, they can be used for treating e.g. traumatic,
ischemic, malignant and degenerative lesions and alcoholic cerebellar
degeneration. Also described is the treatment of lesions associated with
systemic diseases e.g. diabetes or systemic lupus erythematosus, lesions
caused by toxic substances e.g. alcohol, lead or other toxins, and
demyelinated lesions of the nervous system, in which a portion of the
nervous system is destroyed or injured by a demyelinating disease e.g.
multiple sclerosis, HIV-associated myelopathy, transverse myelopathy of
various etiologies, progressive multifocal leukoencephalopathy or central
pontine myelinolysis, or lesions of the central or peripheral nervous
systems. In addition, agents which promote Nr-CAM function can be
promoted to increase growth of animals (e.g. cows, horses, pigs, goats,
deer, chickens) and plants (particularly edible plants, e.g. tomatoes,
melons, lettuce, carrots, potatoes, and other vegetables), particularly
those that are food or material sources. They can also be used in vitro
e.g. to expand cells e.g. stem cells, progenitor cells, muscle cells,
fibroblasts, or liver cells to grow cells/tissue in vitro prior to
administration to a patient. The products can also be used for detection,
diagnosis and production of animal models. The present sequence
represents the nucleotide sequence of the human Nr-CAM gene

Sequence 4134 BP; 1256 A; 904 C; 955 G; 1019 T; 0 U; 0 Other;

Query Match 100.0%; Score 4134; DB 3; Length 4134;
Best Local Similarity 100.0%; Pred. No. 0;

Matches 4134; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CTTCAAGTCCCGCATGAATTAACCTTGACACACAGCTTTCAGAAATCTT 60
1 CTTCAAGTCCCGCATGAATTAACCTTGACACACAGCTTTCAGAAATCTT 60
61 TTGTGAAGAGAAAGAAATTCAGTGTGAGTCTGACAGAGATTAAGTATGAG 120
61 TTGTGAAGAGAAAGAAATTCAGTGTGAGTCTGACAGAGATTAAGTATGAG 120
121 CTTAAATATATGCGAAAGAAAGCGCTTATCTGCGGAGAGATGCCCCGATTCCTTC 180
121 CTTAAATATATGCGAAAGAAAGCGCTTATCTGCGGAGAGATGCCCCGATTCCTTC 180
181 CTGTGCGAGATGATGTGACATGGAATCTTGTATCCAAACCTTCTTGAAGACTTG 240
181 CTGTGCGAGATGATGTGACATGGAATCTTGTATCCAAACCTTCTTGAAGACTTG 240
241 GTACAGCTCCCAACATCAACCAAGCTCTCCAAAGATTACATTATGACCTCGGAG 300
241 GTACAGCTCCCAACATCAACCAAGCTCTCCAAAGATTACATTATGACCTCGGAG 300
301 AATATTTATATCCAGTGTGAAGCCAAAGCCGCCCAAGCTTTCTCGACCCGT 360
301 AATATTTATATCCAGTGTGAAGCCAAAGCCGCCCAAGCTTTCTCGACCCGT 360
361 AATGGAATCTATTTTGAATGAAGACCTCTGTGTCACATGAAGCTTGACAG 420
361 AATGGAATCTATTTTGAATGAAGACCTCTGTGTCACATGAAGCTTGACAG 420
421 AATGGAATCTATTTTGAATGAAGACCTCTGTGTCACATGAAGCTTGACAG 480
421 AATGGAATCTATTTTGAATGAAGACCTCTGTGTCACATGAAGCTTGACAG 480
481 TGTACAGCAAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
481 TGTACAGCAAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
541 AGATCAACATTTGTGAGCAAAAGAAAGCTTGAACCAATCACTTCAAGTGTGCT 600
541 AGATCAACATTTGTGAGCAAAAGAAAGCTTGAACCAATCACTTCAAGTGTGCT 600

601 TTAGTACTTCCCTGAGACCCCAATTTGATTAACCAACCTATATATTTTGATGAT 660
601 TTAGTACTTCCCTGAGACCCCAATTTGATTAACCAACCTATATATTTTGATGAT 660
661 AATTCCTTTCAAGACTTCCACAAAGTGAAGAGATTTCTCAAGTTTGAATGGGACCTT 720
661 AATTCCTTTCAAGACTTCCACAAAGTGAAGAGATTTCTCAAGTTTGAATGGGACCTT 720
721 TATTTTCCAAATGTCTCCGAGAGACCCGCAAGACTATATTTGTTATGCTAGATTT 780
721 TATTTTCCAAATGTCTCCGAGAGACCCGCAAGACTATATTTGTTATGCTAGATTT 780
781 AATCACTCAACCAATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
781 AATCACTCAACCAATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
841 GAATTAATGACATATAGTCTGTAATTTGAGTCACTGAGTTTATGCTGTAATCA 900
841 GAATTAATGACATATAGTCTGTAATTTGAGTCACTGAGTTTATGCTGTAATCA 900
901 AGTGAAG 960
901 AGTGAAG 960
961 TTAAGAGAGAAATGTCTTCACTGAGAGTCAATTTGAGTCACTGAGAGAGAGAG 1020
961 TTAAGAGAGAAATGTCTTCACTGAGAGTCAATTTGAGTCACTGAGAGAGAGAG 1020
1021 TACTGGGCAAG 1080
1021 TACTGGGCAAG 1080
1081 TAAACCTGAGAGATGATTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1140
1081 TAAACCTGAGAGATGATTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1140
1141 AAAAATGATTTAG 1200
1141 AAAAATGATTTAG 1200
1201 TGATGACAG 1260
1201 TGATGACAG 1260
1261 AAGAGTAAATGAG 1320
1261 AAGAGTAAATGAG 1320
1321 ATTGCCCCGATGAG 1380
1321 ATTGCCCCGATGAG 1380
1381 CAAGAAAGATCAAGTGAATATATGATGAGAGAGAGAGAGAGAGAGAGAGAGAG 1440
1381 CAAGAAAGATCAAGTGAATATATGATGAGAGAGAGAGAGAGAGAGAGAGAGAG 1440
1441 GGAAG 1500
1441 GGAAG 1500
1501 CTCTACAGAGTCAATTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1560
1501 CTCTACAGAGTCAATTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1560
1561 GTTCAACATGAG 1620
1561 GTTCAACATGAG 1620
1621 GTTTTAAATGAG 1680
1621 GTTTTAAATGAG 1680

QY 1681 CCTGTGGCCCAAAAAGACAGTACAGGAACCTTATACGTGTGTCGAAGATAAATTAGGG 1740
DB CCTGTGGCCCAAAAAGACAGTACAGGAACCTTATACGTGTGTCGAAGATAAATTAGGG 1740
QY 1741 ATGGCAAAAGATTAAGTCTTACAGCCCGAATATGCACTGTTGTGCAAAAGAGGACATG 1800
DB 1741 ATGGCAAAAGATTAAGTCTTACAGCCCGAATATGCACTGTTGTGCAAAAGAGGACATG 1800
QY 1801 GTGTCTTTGAATGCAAGTGAAGATGATACACCTTATCCCTCACTGTGCTGTGGCTG 1860
DB 1801 GTGTCTTTGAATGCAAGTGAAGATGATACACCTTATCCCTCACTGTGCTGTGGCTG 1860
QY 1861 AAGGACAAAGAGGAGCTGCGCAGTGAATGAAGGTTGACTGTTGCAAGATCATCTAGTG 1920
DB 1861 AAGGACAAAGAGGAGCTGCGCAGTGAATGAAGGTTGACTGTTGCAAGATCATCTAGTG 1920
QY 1921 GTTACTGATGTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1980
DB 1921 GTTACTGATGTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1980
QY 1981 GACAGGTCTCCGCGCAGGCTGTGCTTGAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTG 2040
DB 1981 GACAGGTCTCCGCGCAGGCTGTGCTTGAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTG 2040
QY 2041 GTTTACGATGTCCCAATCTCTCCCTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 2100
DB 2041 GTTTACGATGTCCCAATCTCTCCCTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 2100
QY 2101 GTTACAGCTGTCAATGACCCCGAGGATGACAAATAGCCCTTGAAGTGAAGTGAAGTGA 2160
DB 2101 GTTACAGCTGTCAATGACCCCGAGGATGACAAATAGCCCTTGAAGTGAAGTGAAGTGA 2160
QY 2161 GAATATGAAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2220
DB 2161 GAATATGAAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2220
QY 2221 AACACAGACCAAGCCAGCTGAAGTGTCTCTTGAAGTGAAGTGAAGTGAAGTGAAGTGA 2280
DB 2221 AACACAGACCAAGCCAGCTGAAGTGTCTCTTGAAGTGAAGTGAAGTGAAGTGAAGTGA 2280
QY 2281 GAGTGAACAGCATTTGGAAAGCTTGGCCAGGAGGCTGTGAGCATTAATTTGAGAA 2340
DB 2281 GAGTGAACAGCATTTGGAAAGCTTGGCCAGGAGGCTGTGAGCATTAATTTGAGAA 2340
QY 2341 GCTTGAACAGCATTAATTTGAGAAAGCTTGGCCAGGAGGCTGTGAGCATTAATTTGAGAA 2400
DB 2341 GCTTGAACAGCATTAATTTGAGAAAGCTTGGCCAGGAGGCTGTGAGCATTAATTTGAGAA 2400
QY 2401 TTGAGATTAAGTGAAGCTTGAATGATGATGATGATGATGATGATGATGATGATGATG 2460
DB 2401 TTGAGATTAAGTGAAGCTTGAATGATGATGATGATGATGATGATGATGATGATGATG 2460
QY 2461 AAAGTTAGTGGGCGCAGAAAGATGATGATGATGATGATGATGATGATGATGATGATG 2520
DB 2461 AAAGTTAGTGGGCGCAGAAAGATGATGATGATGATGATGATGATGATGATGATGATG 2520
QY 2521 GTATCCAAATTAATTTGTCTCAGGACAGCACTTGTCTCATCTGATCAAAAGTTGAG 2580
DB 2521 GTATCCAAATTAATTTGTCTCAGGACAGCACTTGTCTCATCTGATCAAAAGTTGAG 2580
QY 2581 GGCCTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2640
DB 2581 GGCCTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2640
QY 2641 GACCTTCCCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2700
DB 2641 GACCTTCCCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2700
QY 2701 GAGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2760
DB 2701 GAGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2760
QY 2761 ATTACTATTGAAAGACAGATTCATTAAGAAAGACAGATTCATTAAGAAAG 2820

DB 2761 ATTACTATTGAAAGACAGATTCATTAAGAAAGACAGATTCATTAAGAAAG 2820
QY 2821 ATTCCTACCTTCCAGGACAGATTCATTAAGAAAGACAGATTCATTAAGAAAG 2880
DB 2821 ATTCCTACCTTCCAGGACAGATTCATTAAGAAAGACAGATTCATTAAGAAAG 2880
QY 2881 CACTACACACTGAATGTCCAGTGTGCTCAATGGAAGAGGAGGAGGAGGAGGAGGAGGAGG 2940
DB 2881 CACTACACACTGAATGTCCAGTGTGCTCAATGGAAGAGGAGGAGGAGGAGGAGGAGGAGG 2940
QY 2941 AGAGTCTTTAATTAATTCAGAAAGAGTCCCAAGTGTCCCTGCTGCTTGAAGATGATG 3000
DB 2941 AGAGTCTTTAATTAATTCAGAAAGAGTCCCAAGTGTCCCTGCTGCTTGAAGATGATGATG 3000
QY 3001 CCACACAGTGAATCTCTCACTTGTGGAATGGAATCCACGAGGACCCGAGTGGCATTTTG 3060
DB 3001 CCACACAGTGAATCTCTCACTTGTGGAATGGAATCCACGAGGACCCGAGTGGCATTTTG 3060
QY 3061 ACAGATGACCTTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3120
DB 3061 ACAGATGACCTTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3120
QY 3121 GATTTGAATTAATTCCTGCAACAGACAGGATGATGATGATGATGATGATGATGATGATG 3180
DB 3121 GATTTGAATTAATTCCTGCAACAGACAGGATGATGATGATGATGATGATGATGATGATG 3180
QY 3181 GATTTGAATTAATTCCTGCAACAGACAGGATGATGATGATGATGATGATGATGATGATG 3240
DB 3181 GATTTGAATTAATTCCTGCAACAGACAGGATGATGATGATGATGATGATGATGATGATG 3240
QY 3241 GAAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3300
DB 3241 GAAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3300
QY 3301 GTTCAAGCTGTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 3360
DB 3301 GTTCAAGCTGTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 3360
QY 3361 AATATCAGTGTGGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3420
DB 3361 AATATCAGTGTGGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3420
QY 3421 GAGGACAGCAAGAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3480
DB 3421 GAGGACAGCAAGAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3480
QY 3481 TTAAGAGGTCTAATCCAGAAACAGCATTAAGTTCAGATGATGATGATGATGATGATGATG 3540
DB 3481 TTAAGAGGTCTAATCCAGAAACAGCATTAAGTTCAGATGATGATGATGATGATGATGATG 3540
QY 3541 GGTTTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3600
DB 3541 GGTTTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3600
QY 3601 GATATGCACTCAGAGGCTGTGCTAATGATGATGATGATGATGATGATGATGATGATGATG 3660
DB 3601 GATATGCACTCAGAGGCTGTGCTAATGATGATGATGATGATGATGATGATGATGATGATG 3660
QY 3661 ATTTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3720
DB 3661 ATTTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3720
QY 3721 AAGGAAAGTGTCCATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 3780
DB 3721 AAGGAAAGTGTCCATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 3780
QY 3781 GAGGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3840
DB 3781 GAGGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3840
QY 3841 GACAGACTGTGAAAGAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3900

Db 3841 GACAGACTGTGTAAGAAAAGATAGTACGACAGCCTAGTACTATGAGAGAGGGGTT 3900
 QY 3901 AATGGCACTTCAATAGATAGCTCTTATTTGACATATACAGTGTAGAAAGGAA 3960
 Db 3901 AATGGCACTTCAATAGATAGCTCTTATTTGACATATACAGTGTAGAAAGGAA 3960
 QY 3961 GAGCCGCTGAAAGAAAGAGCTCAGAGGACCTTCTCTGTCACGCCATGATTC 4020
 Db 3961 GAGCCGCTGAAAGAAAGAGCTCAGAGGACCTTCTCTGTCACGCCATGATTC 4020
 QY 4021 TTTGTTTAAATTTTAAAGCTCAAGCCATATTTCTCTAGATTTTATCTTAC 4080
 Db 4021 TTTGTTTAAATTTTAAAGCTCAAGCCATATTTCTCTAGATTTTATCTTAC 4080
 QY 4081 TCTGTTTGTGAGCCCTCTCATATCTATGAAATATGAGTATATTTTC 4134
 Db 4081 TCTGTTTGTGAGCCCTCTCATATCTATGAAATATGAGTATATTTTC 4134
 RESULT 2
 ID AAV62739 standard; cDNA; 3997 BP.
 XX AAV62739;
 AC
 XX
 DT 02-FEB-1999 (first entry)
 XX
 DE Human neural cell adhesion molecule NRCAMvar cDNA.
 XX
 KW NRCAMvar; NRCAM; neural cell adhesion molecule; human; diabetes; obesity;
 XX cancer; therapy; diagnosis; vaccine; ss.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT CDS 18..3932
 FT /*tag= a
 XX
 PN MO9836062-A1.
 XX
 PD 20-AUG-1998.
 XX
 PF 12-FEB-1998; 98WO-GB000434.
 XX
 PR 13-FEB-1997; 97GB-00003011.
 PR 22-JUL-1997; 97EB-00305485.
 XX
 PA (SMK) SMITHKLINE BEECHAM PLC.
 XX
 PI Terrett JA, Kenwick SJ, Wang B;
 XX
 DR WPI, 1998-520757/44.
 DR P-PSDB; AAM59994.
 XX
 PT NRCAM-related cell adhesion molecule splice variant polypeptide NRCAMvar
 PS - used to treat diabetes, obesity and cancer.
 PS Claim 4; Page 20-22; 32pp; English.
 XX
 CC This is the nucleotide sequence of a cDNA clone encoding a splice
 CC variant, designated NRCAMvar (see AAM59994), of human neural cell
 CC adhesion molecule NRCAM. The HGS EST database was screened using the
 CC chick NRCAM sequence, and 3 EST clones were obtained from human adrenal
 CC and striatum cDNA libraries. Fragments homologous to NRCAM were end-
 CC sequenced and used as probes to screen a human foetal brain cDNA library.
 CC 4 Positive clones were isolated and inserts were subcloned into
 CC pBluescript plasmids. Additional sections of the gene were isolated using
 CC gene-specific primers to amplify cDNA from human foetal brain libraries.
 CC The DNA sequence of human NRCAMvar is 77.1% identical to that of the
 CC chick gene. NRCAMvar polypeptides and polynucleotides are disclosed of
 CC producing such polypeptides by recombinant techniques and methods of
 CC disclosed are methods for utilising such polypeptides and polynucleotides
 CC in the design of protocols for the treatment of conditions associated

CC with NRCAM imbalance, including diabetes, obesity and cancer, as well in
 CC diagnostic assays for such conditions, and in vaccines. The nucleotide
 CC sequence can be used to diagnose diseases caused by a mutation of the
 CC NRCAMvar polypeptide or to screen a library for NRCAMvar homologues
 XX
 SQ Sequence 3997 BP; 1203 A; 888 C; 928 G; 978 T; 0 U; 0 Other;
 Query Match 90.7%; Score 3751.6; DB 2; Length 3997;
 Best Local Similarity 97.0%; Pred. No. 0;
 Matches 3867; Conservative 0; Mismatches 59; Indels 60; Gaps 2;
 QY 103 GAGATTAAAGCTATGACAGCTTAAATTAATGCGGAAAAAGAGCGCTTATTCGGGGGAGA 162
 Db 6 GTAATTCGCTTAATCAGCTTAAATTAATGCGGAAAAAGAGCGCTTATTCGGGGGAGA 65
 QY 163 GTGGCCCTGATCTCTCTCTGCGAGATGATTAAGTACGTAGAGTACCTTATGATCA 222
 Db 66 GTGGCCCTGATCTCTCTCTGCGAGATGATTAAGTACGTAGAGTACCTTATGATCA 125
 QY 223 AAATCTTGAAGACTGTGATACAGCTCCAAACCATCAACCAAGCTCTCAAAAGATTAC 282
 Db 126 AAATCTTGAAGACTGTGATACAGCTCCAAACCATCAACCAAGCTCTCAAAAGATTAC 185
 QY 283 ATTATTAACCTCGGAGAAATTTGTAAATCCAGTGTGAAGCCAAAGGAAACCGCCCCA 342
 Db 186 ATTATTAACCTCGGAGAAATTTGTAAATCCAGTGTGAAGCCAAAGGAAACCGCCCCA 245
 QY 343 AGCTTTCTGTGACCCGTAATGAGGACTCATTTTGCATGATTAAGACCTCTGTGTCAC 402
 Db 246 AGCTTTCTGTGACCCGTAATGAGGACTCATTTTGCATGATTAAGACCTCTGTGTCAC 305
 QY 403 ATGAAGCCTGACAGAAAGCTCATTAATTAATCATATGAGGAAAGGAAAGCTGAGAC 462
 Db 306 ATGAAGCCTGACAGAAAGCTCATTAATTAATCATATGAGGAAAGGAAAGCTGAGAC 365
 QY 463 TATGAAGAGTCTATCAGTGTACAGAAAGAAAGAAAGGAAAGGAAAGGAAAGGAAAG 522
 Db 366 TATGAAGAGTCTATCAGTGTACAGAAAGAAAGGAAAGGAAAGGAAAGGAAAGGAAAG 425
 QY 523 ATTGTTCGCGCCATCCAGATCACATTTGAGGACCAAAAGAAAGGAAAGGAAAGGAAAG 582
 Db 426 ATTGTTCGCGCCATCCAGATCACATTTGAGGACCAAAAGAAAGGAAAGGAAAGGAAAG 485
 QY 583 CTTCAAAGTGTACAGTCTTATGATCTCTCCAGAGACCCCAATTGATTAACACACCT 642
 Db 486 CTTCAAAGTGTACAGTCTTATGATCTCTCCAGAGACCCCAATTGATTAACACACCT 545
 QY 643 ATTAATATTTGGATGATTAATCTTTTCAAGACTTCCAAAGAGTGAAGAGTTTCTCA 702
 Db 546 ATTAATATTTGGATGATTAATCTTTTCAAGACTTCCAAAGAGTGAAGAGTTTCTCA 605
 QY 703 GGTTCGATGAGGAGCCTTATTTTCAATGCTCCAGAGGACCCGAGAGACTAT 762
 Db 606 GGTTCGATGAGGAGCCTTATTTTCAATGCTCCAGAGGACCCGAGAGACTAT 665
 QY 763 ATCTGTTATGCTAGATTTATATCATCTCAACCATACAGAGAAAGAAAGCTTATCTG 822
 Db 666 ATCTGTTATGCTAGATTTATATCATCTCAACCATACAGAGAAAGAAAGCTTATCTG 725
 QY 823 AAGTGATTTCAAGTGAATGAATGACATTAAGTCTGTAATTTGAGTACCTGAG 882
 Db 726 AAGTGATTTCAAGTGAATGAATGACATTAAGTCTGTAATTTGAGTACCTGAG 785
 QY 883 TTTTATGCTCAATTAATCAAGTGAAGAGGACCAACATTTTAACTCCAGAGGCAAT 942
 Db 786 TTTTATGCTCAATTAATCAAGTGAAGAGGACCAACATTTTAACTCCAGAGGCAAT 845
 QY 943 GCAAGTAAAGAGAAATTAAGAGAAATGCTTCACTGAGTGTGACAGAGGA 1002
 Db 846 GCAAGTAAAGAGAAATTAAGAGAAATGCTTCACTGAGTGTGACAGAGGA 905
 QY 1003 GTGCTTACCCCAATTATTTACTGGGCAAGAGAGTGAATCTTACCAAAACAGAGACA 1062

Db	966	CTGCCTACCCCAATTATTACTGCGGCAGAAAGGATGGAATGCTAACCCAAAGAACAGCA	965
OY	1063	GTTATATAAGAACTTTGAGAAAACTTGCAGATCATTCATGTTTTCAGAAAGCACTCTGGA	11222
Db	966	GTTATATAAGAACTTTGAGAAAACTTGCAGATCATTCATGTTTTCAGAAAGCACTCTGGA	10251
OY	1123	AATTACCAATGTATPAGCAAAAAATGCATTTAGAGCAATCCACATCACTTTCTGTAGA	1182
Db	1026	AATTACCAATGTATPAGCAAAAAATGCATTTAGAGCAATCCACATCACTTTCTGTAGA	1085
OY	1183	GTTAAAGGGCGCTCCATCTGTGATCAGACCCCTCAAAATCTTGTCGTCTCCCGAGAGAG	12424
Db	1086	GTTAAAGGGCGCTCCATCTGTGATCAGACCCCTCAAAATCTTGTCGTCTCCCGAGAGAG	1145
OY	1243	GATGGAGCTTTGATCTGAGAGCTAATGSCAAACCCCAACCCAGAAATTAGCTGTAAACA	13020
Db	1146	GATGGAGCTTTGATCTGAGAGCTAATGSCAAACCCCAACCCAGAAATTAGCTGTAAACA	1205
OY	1303	AATGAGTCCCAATPAGAAATTTGCCCTGATGATCCCGACAGAAAAATPAGATGGGATACC	1362
Db	1206	AATGAGTCCCAATPAGAAATTTGCCCTGATGATCCCGACAGAAAAATPAGATGGGATACC	1265
OY	1363	ATTATTTTTTCAAAATGTTCAAGAAAAGATCAAGTGCAGATATPACATGTCATGCTCTAAT	14222
Db	1266	ATTATTTTTTCAAAATGTTCAAGAAAAGATCAAGTGCAGATATPACATGTCATGCTCTAAT	1325
OY	1423	GAATATGAGATATTTACTGSCAAACGCAATTTGTAAATGTCTGCGCTGAGCCACACGATC	1482
Db	1326	GAATATGAGATATTTACTGSCAAACGCAATTTGTAAATGTCTGCGCTGAGCCACACGATC	1385
OY	1483	CTCACACCTGCAAACACACTCTACCAAGTCAATTGCAACAGGCTGCTTTACTGATCTGT	1542
Db	1386	CTCACACCTGCAAACACACTCTACCAAGTCAATTGCAACAGGCTGCTTTACTGATCACTGT	1445
OY	1543	GCGTTCTTTGGGTCTCCTCCCAACCATGAGTGTAAAGAGCTAAAGGAAGTGC	1602
Db	1446	GCGTTCTTTGGGTCTCCTCCCAACCATGAGTGTAAAGAGCTAAAGGAAGTGC	1505
OY	1603	CTTCATGAAAGATATTATGTATTACATGAAATGGAACCTTGGAAATCAAGATGCTACA	1662
Db	1506	CTTCATGAAAGATATTATGTATTACATGAAATGGAACCTTGGAAATCAAGATGCTACA	1547
OY	1663	TGATCGTTAAAGAAATTCCTGTGGCCCAAAAGGACAGTACAGAACTTATACGTGT	1722
Db	1548	TGATCGTTAAAGAAATTCCTGTGGCCCAAAAGGACAGTACAGAACTTATACGTGT	1595
OY	1723	GCAAGGAATTAATTAAGGATGGCAAGAAATGAATCTT-----	1763
Db	1596	GCAAGGAATTAATTAAGGATGGCAAGAAATGAATCTTAAAGATCTTACA	1655
OY	1764	-----ACAGCCGGAATATGCAATTTGCAAAAGGAGCAATGCTCTTTGAA	1812
Db	1656	TGATCGTTAAACAGCCCGGAATATGCAATTTGCAAAAGGAGCAATGCTCTTTGAA	1715
OY	1813	TGCAAAAGTGAACATGATCAACCTTATCCCTCACTGTCTGTGGCTGAAAGACACAGG	1872
Db	1716	TGCAAAAGTGAACATGATCAACCTTATCCCTCACTGTCTGTGGCTGAAAGACACAGG	1775
OY	1873	GAACTGCCCAATGTAAGAAAGGTACCTGTGTACAGGAATCATATAGTGTAGCTGATGTC	1932
Db	1776	GAACTGCCCAATGTAAGAAAGGTACCTGTGTACAGGAATCATATAGTGTAGCTGATGTC	1835
OY	1933	AGTGACATGACAGCGGAGCTTACACGTGTGGCCAAACCACTTGGACAGGCTTCC	1992
Db	1836	AGTGACATGACAGCGGAGCTTACACGTGTGGCCAAACCACTTGGACAGGCTTCC	1895
OY	1993	GCCAGCGCTGCTTAAAGGCTTGTGCTCTTACCTCAACTCCAGCTCCCGTTACGATGTC	2052
Db	1896	GCCAGCGCTGCTTAAAGGCTTGTGCTCTTACCTCAACTCCAGCTCCCGTTACGATGTC	1955
OY	2053	CCAAATCTCTCTTGAATGTAACATGACAAATCTTGAACAAAGTTCACACTGTCA	2112
Db	1956	CCAAATCTCTCTTGAATGTAACATGACAAATCTTGAACAAAGTTCACACTGTCA	2015

QY	2113	TTGACCCGAGCGATGACCAACAATAGGCCATTTACAAATTCATCATCGAATATGAAAT	2112
Db	2016	TGACCCCGCATGACACACATAGCCCATTTACAAATTCATGACGAATATGAAAT	2075
QY	2173	GCAATGCAACAAGCCAGGGCTGTGGCACACCAACTGAAGTTCTGGACAACAGACCA	2232
Db	2076	GCAATGCAACAAGCCAGGGCTGTGGCACCAACCAACTGAAGTTCTGGACAACAGACCA	2135
QY	2223	GGCCAGCTGAAAGCTGTCTCTTACGTAACTACTCTCCGCGTAGTGGCAATGAAACAGC	2292
Db	2136	GGCCAGCTGAAAGCTGTCTCTTACGTAACTACTCTCCGCGTAGTGGCAATGAAACAGC	2195
QY	2293	ATTGGGAAAGACTTGCACGAGGCGCTCTGAGCAGTATTTGACGAAGGCTCGAAGACA	2352
Db	2196	ATTGGGAAAGACTTGCACGAGGCGCTCTGAGCAGTATTTGACGAAGGCTCGAAGACA	2255
QY	2353	GATTAACAAACCCCAAGCTGTGGAAAGACTGGGAATCAAGCTCTGATAATTGGAGATTACG	2412
Db	2256	GATTAACAAACCCCAAGCTGTGGAAAGACTGGGAATCAAGCTCTGATAATTGGAGATTACG	2315
QY	2413	TGAAAGCCCTTGAAATGGTTTGAAATCTAATGGGCGAGGCTTCAGTACAAAGTTAGCTGG	2472
Db	2316	TGAAAGCCCTTGAAATGGTTTGAAATCTAATGGGCGAGGCTTCAGTACAAAGTTAGCTGG	2375
QY	2473	CGCCAGAAAGATGATGTGATGAAATGGAACATCTGTGTTGTGGCAATGTATCCAAATAT	2532
Db	2376	CGCCAGAAAGATGATGTGATGAAATGGAACATCTGTGTTGTGGCAATGTATCCAAATAT	2435
QY	2533	ATTGTCTCAGGCAAGCCCACTTTGTTCCATCTGATCAAAAGTTCAGGCGCTGAAAGAC	2592
Db	2436	ATTGTCTCAGGCAAGCCCACTTTGTTCCATCTGATCAAAAGTTCAGGCGCTGAAAGAC	2495
QY	2593	ATGGGGTTTGGCCCGGACGACGCTGTAGTACATGAGGAATTTCTGGAGAAAGACTTCCCATG	2652
Db	2496	ATGGGGTTTGGCCCGGACGACGCTGTAGTACATGAGGAATTTCTGGAGAAAGACTTCCCATG	2555
QY	2653	GTGCTCTCTGGGAACGTGCGTGTGATGTGTGAAACGTACCTTAGCCGAGGTCCACTGG	2712
Db	2556	GTGCTCTCTGGGAACGTGCGTGTGATGTGTGAAACGTACCTTAGCCGAGGTCCACTGG	2615
QY	2713	GACCCAGTACCTCGAAGAAAGATCCGAGGACACCTTAAGGCTATGGATTTTACTATTGG	2772
Db	2616	GACCCAGTACCTCGAAGAAAGATCCGAGGACACCTTAAGGCTATGGATTTTACTATTGG	2675
QY	2773	AAGACCCAGAGTTTATCTAATAAGAAACAGACGTTCACATTGAGAAAAAGATCCTCACCTTC	2832
Db	2676	AAGACCCAGAGTTTATCTAATAAGAAACAGACGTTCACATTGAGAAAAAGATCCTCACCTTC	2735
QY	2833	CAAGGCAAGCAAGATCTATGCGCATGTGTGCGGGGCTAAGCCCTTTACCACTACACACTG	2892
Db	2736	CAAGGCAAGCAAGATCTATGCGCATGTGTGCGGGGCTAAGCCCTTTACCACTACACACTG	2795
QY	2893	AATGTCCGAGTGTTCATATGGGAAAGGGAAGGACCCACACGACCTGTGACAGAGTCTTTAAT	2952
Db	2796	AATGTCCGAGTGTTCATATGGGAAAGGGAAGGACCCACACGACCTGTGACAGAGTCTTTAAT	2855
QY	2953	ACTCCAGAAGAGTCTCCCAAGTGTCTCCTCGTCTTTGAAGATTGTGAATCCACACTGGAC	3012
Db	2856	ACTCCAGAAGAGTCTCCCAAGTGTCTCCTCGTCTTTGAAGATTGTGAATCCACACTGGAC	2915
QY	3013	TCTCTCATCTTTGGAATGGGATCCACCGAGGCCACCGAATGGCATTTTGAACAGAGTACACC	3072
Db	2916	TCTCTCATCTTTGGAATGGGATCCACCGAGGCCACCGAATGGCATTTTGAACAGAGTACACC	2975
QY	3073	TTAAAGTATCAGCCCAATTTAACAGACACATGAATTAGGCGCTCTGTGATATTTGAAATTT	3132
Db	2976	TTAAAGTATCAGCCCAATTTAACAGACACATGAATTAGGCGCTCTGTGATATTTGAAATTT	3035
QY	3133	CTTGGCAACAAGACAGGTGCACTTTTAAAAAATTTTAAATTTTCACTCGATATTAAGTTT	3192
Db	3036	CTTGGCAACAAGACAGGTGCACTTTTAAAAAATTTTAAATTTTCACTCGATATTAAGTTT	3095

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QY 3193 TATTTCTATGACAAACATCAGAGATCAGAGAGTCAATTAACAGAGAGAGAGTAAACA 3252
DB 3096 TATTTCTATGACAAACATCAGAGATCAGAGAGTCAATTAACAGAGAGAGAGTAAACA 3155
QY 3253 ACTGTGATGAGAGCTGTATTTCTTCCACTGATGAGTGGGACGAGAGTCAAGCTGTA 3312
DB 3156 ACTGTGATGAGAGCTGTATTTCTTCCACTGATGAGTGGGACGAGAGTCAAGCTGTA 3215
QY 3313 AATACAGAGATCAGAGATCTTACTGCTGAGCTGAGAGCCATGAGCCAAATCAATGAGT 3372
DB 3216 AATCCAGAGATCAGAGATCTTACTGCTGAGCTGAGAGCCATGAGCCAAATCAATGAGT 3275
QY 3373 GAATATGAGGAGCAGAGAGATGAGACTTTTATGTTGAATATGTTGATGAGGACGACAA 3432
DB 3276 GAATATGAGGAGCAGAGAGATGAGACTTTTATGTTGAATATGTTGATGAGGACGACAA 3335
QY 3433 GAAGATGAGAGAGAGAGAGATGTTAAATGTTCTGAGAGCTTTCTTGGTTAAAGGATCTA 3492
DB 3336 GAAGATGAGAGAGAGAGAGATGTTAAATGTTCTGAGAGCTTTCTTGGTTAAAGGATCTA 3395
QY 3493 ATGCCAGAGAACAGCATACAAAGTTGAGTTGCTGAGGAGGAGCTCTGAGTTTGTGAGT 3552
DB 3396 ATGCCAGAGAACAGCATACAAAGTTGAGTTGCTGAGGAGGAGCTCTGAGTTTGTGAGT 3455
QY 3553 TCAGAGATGTTGTTGAGACAGGCCAGAGATGAGAGCCGAGAGTGAATATGAGCACT 3612
DB 3456 TCAGAGATGTTGTTGAGACAGGCCAGAGATGAGAGCCGAGAGTGAATATGAGCACT 3515
QY 3613 CAGGGCTGTTCTATTTGCTGATGTTGCTGCTCTCTCTTATCTTAAATTTTGTGAGT 3672
DB 3516 CAGGGCTGTTCTATTTGCTGATGTTGCTGCTCTCTCTTATCTTAAATTTTGTGAGT 3575
QY 3673 GTTTGCTTATCAGAGAGAGAGAGGTTGTAATATCCAGTTAAAGAGAGAGATGAGC 3732
DB 3576 GTTTGCTTATCAGAGAGAGAGAGGTTGTAATATCCAGTTAAAGAGAGAGATGAGC 3635
QY 3733 CATGTGACCTCTGAATTCAGCTTATGAGAGAGATGAGGACATTTGAGAGATACAGT 3792
DB 3636 CATGTGACCTCTGAATTCAGCTTATGAGAGAGATGAGGACATTTGAGAGATACAGT 3695
QY 3793 GATGCAAGAGACCAAGCCTTTGAAAAAGAGAGTGAATCTCTTCAACAGAGACTGTG 3852
DB 3696 GATGCAAGAGACCAAGCCTTTGAAAAAGAGAGTGAATCTCTTCAACAGAGACTGTG 3755
QY 3853 AAAAAAGAGATGAGACAGACAGCTTATGAGAGAGAGGTTATGAGCCAGTTC 3912
DB 3756 AAAAAAGAGATGAGACAGACAGCTTATGAGAGAGAGGTTATGAGCCAGTTC 3815
QY 3913 AATGAGATGAGCTCTTTATGAGACATACAGTGTAGAGAGAGAGAGCCGAGCTGAA 3972
DB 3816 AATGAGATGAGCTCTTTATGAGACATACAGTGTAGAGAGAGAGAGCCGAGCTGAA 3875
QY 3973 GGAAGAGAGAGCTCAGAGAGCCTTCTCTGTCAGAGCCATGAGTTCTTTTATTT 4032
DB 3876 GGAAGAGAGAGCTCAGAGAGCCTTCTCTGTCAGAGCCATGAGTTCTTTTATTTATCA 3935
QY 4033 TTAAGCTCAAGCCATATTCATTT 4058
DB 3936 TAGAATTGATTCGATGATGCTTT 3961

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RESULT 3
AAA64155
ID AAA64155 standard; cdna; 6253 BP.
XX
XX AAA64155;
AC
XX
XX 20-DEC-2000 (first entry)
DT
XX
XX Nucleotide sequence of secreted protein clone C0722_1.
DE
XX
XX Human; secreted protein; immune deficiency; infectious disease;
KW tissue growth; wound healing; tissue repair; burn; incision; ulcer;

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KW osteoporosis; osteoarthritis; periodontal disease; tooth repair;
KW nervous system disorder; angiogenic activity; fibrosis; fertility;
KW reperfusion injury; systemic cytokine damage; contraceptive;
KW thrombolytic; coagulation disorder; antiinflammatory activity;
KW inflammatory condition; ss.
XX
XX Homo sapiens.
FH Key Location/Qualifiers
FT CDS 383..396
FT /tag=a
FT /product="secreted protein"
XX
XX WO20050592-A1.
XX
XX 31-AUG-2000.
XX
XX 24-FEB-2000; 2000WO-US004731.
XX
XX 24-FEB-1999; 99US-00256938.
XX
XX (GENV) GENETICS INST INC.
XX
XX Jacobs K, McCoy JM, Lavalie ER, Collins-Racie LA, Evans C;
XX Merberg D, Treacy M, Bowman MR, Spaulding V;
XX
XX MPI: 2000-558399/51.
XX
XX P-PsDB; AAB08442.
XX
XX
XX New secreted polypeptides and nucleic acids encoding them used for
XX treating various anemias, bone, cartilage, tendon, ligament and/or nerve
XX tissue or regeneration, contraceptives, and nutritional supplements.
XX
XX Disclosure; Page 104-105; 11pp; English.
XX
XX
XX The present sequence encodes a human secreted protein. The polypeptides
XX may be used in the treatment of various immune deficiencies and
XX disorders, and to treat infectious diseases caused by viral, bacterial,
XX fungal or other infections. The polypeptides are also used in
XX compositions for bone, cartilage, tendon, ligament and/or nerve tissue
XX growth or regeneration, for wound healing and tissue repair and
XX replacement, and in the treatment of burns, incisions and ulcers. The
XX protein is used in the treatment of osteoporosis or osteoarthritis,
XX periodontal disease and other tooth repair processes, and nervous system
XX disorders. They also exhibit angiogenic activity and protect, regenerate
XX and treat lung or liver fibrosis, reperfusion injury in various tissues,
XX and conditions resulting from systemic cytokine damage. They promote or
XX inhibit tissue differentiation and are used as contraceptives and to
XX enhance fertility. They also have a hemostatic or thrombolytic activity
XX and can be used to treat various coagulation disorders. They also have an
XX antiinflammatory activity and can be used to treat inflammatory
XX conditions
XX
XX Sequence 6253 BP; 1978 A; 1274 C; 1292 G; 1704 T; 0 U; 5 Other;
XX
XX
XX Query Match 80.2%; Score 3316; DB 3; Length 6253;
XX Best local similarity 90.2%; Pred. No. 0;
XX Matches 3758; Conservative 0; Mismatches 10; Indels 396; Gaps 4;
QY 1 CTTCAAAGTCCCGCATGAAATTAATTACTTAAACGTTGACACACAGCTTTCAGAAATCTT 60
DB 269 CTTCAAAGTCCCGCATGAAATTAATTACTTAAACGTTGACACACAGCTTTCAGAAATCTT 328
QY 61 TTGTGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
DB 329 TTGTGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 388
QY 121 CTTAAATATATCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
DB 389 CTTAAATATATCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 448
QY 181 CTGTCCAGATGATTAGTGCAGTGGAGTACTCTTGATCCAAAACCTTGAAGACTTG 240

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Db 449 CTGTCCAGATGATTAGTCACTGGAAGTACTCTTGTATCCAAACTCTTGAAGACTTG 508
 Qy 241 GTACAGCCTCCAAACATCAACCAACAGTCTCCAAAGATTACATTATGACCTCGGAG 300
 Db 509 GTACAGCCTCCAAACATCAACCAACAGTCTCCAAAGATTACATTATGACCTCGGAG 568
 Qy 301 AATATTGTAATCCAGTGTGAAGCCAAAGGAAACCGCCCCCAAGCTTTTCTGGAACCGT 360
 Db 569 AATATTGTAATCCAGTGTGAAGCCAAAGGAAACCGCCCCCAAGCTTTTCTGGAACCGT 628
 Qy 361 AATGGACATCTTTTACATTCATTAAGACCTCTGTGTACCATGAGCTGGACAGAGA 420
 Db 629 AATGGACATCTTTTACATTCATTAAGACCTCTGTGTACCATGAGCTGGACAGAGA 688
 Qy 421 ACGCTCATATTAAACATCATGAGCGAAGGAAAGCTGAGACCTATGAGAGATCTATCAG 480
 Db 689 ACGCTCATATTAAACATCATGAGCGAAGGAAAGCTGAGACCTATGAGAGATCTATCAG 748
 Qy 481 TGTACAGAGAAAGCAAGCGGAGCTGCAATTCTAATTAACATTTGTGTCCGCCATCC 540
 Db 749 TGTACAGAGAAAGCAAGCGGAGCTGCAATTCTAATTAACATTTGTGTCCGCCATCC 808
 Qy 541 AGATCCATCTTTGGACCAAGAAAATTGAAACATCACTTCAAGTGTGACGTCT 600
 Db 809 AGATCCATCTTTGGACCAAGAAAATTGAAACATCACTTCAAGTGTGACGTCT 868
 Qy 601 TTAGTACTCCCTGAGACCCCAATTGATTAACCACTTAACTAATTTTGGAGAT 660
 Db 869 TTAGTACTCCCTGAGACCCCAATTGATTAACCACTTAACTAATTTTGGAGAT 928
 Qy 661 AATTCCTTTCAAGACTTCCAAAGTGAAGAGATTCTCAAGTGTGAATGGAGCTT 720
 Db 929 AATTCCTTTCAAGACTTCCAAAGTGAAGAGATTCTCAAGTGTGAATGGAGCTT 988
 Qy 721 TATTTTCCAAATGTCTCCCAAGAGACACCCCGAAGACTATATCTGTATGTAGATT 780
 Db 989 TATTTTCCAAATGTCTCCCAAGAGACACCCCGAAGACTATATCTGTATGTAGATT 1048
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 Db 1049 AATCATCTCAACCATATAGAGAGAAAGCAATTTCTGTGAAGTGAATTCAGTGAT 1102
 Qy 841 GAATTGAATGACATATAGCTGTATTTGAGTGAACACTGAGTTTATGTCTAATATCA 900
 Db 1103 -----GCTAATATCA 1111
 Qy 901 AGTAGAGAGGCGCCAAACATTTTAACTCCAGAAAGCAATGCAATGAACAAAGAGAA 960
 Db 1112 AGTAGAGAGGCGCCAAACATTTTAACTCCAGAAAGCAATGCAATGAACAAAGAGAA 1171
 Qy 961 TTAAGAGAAATGTGCTTCACTGAGTGCATTTGCAAGAGACTGTGCTACCCCAATATT 1020
 Db 1172 TTAAGAGAAATGTGCTTCACTGAGTGCATTTGCAAGAGACTGTGCTACCCCAATATT 1231
 Qy 1021 TACTGGGCAAGAGAGATGGAATGTACCCAAAGAAAGAGAGAGTTTATGAAGCTTTGAG 1080
 Db 1232 TACTGGGCAAGAGAGATGGAATGTACCCAAAGAAAGAGAGAGTTTATGAAGCTTTGAG 1291
 Qy 1081 AAAACCTTGAGATCATTTGATGTTTCAAGAGAGACTGTGAATTTCAATGTATAGCA 1140
 Db 1292 AAAACCTTGAGATCATTTGATGTTTCAAGAGAGACTGTGAATTTCAATGTATAGCA 1351
 Qy 1141 AAAATGCAATTAGAGGCTTCCACATTCATTTCTGTGAAGTTTAAAGGCTGCATATC 1200
 Db 1352 AAAATGCAATTAGAGGCTTCCACATTCATTTCTGTGAAGTTTAAAGGCTGCATATC 1411
 Qy 1201 TGGATCAAGCCCTCAAAATCTTGTGTGTCTCCCAAGAGAGATGGAGCTTTGATCTGC 1260
 Db 1412 TGGATCAAGCCCTCAAAATCTTGTGTGTCTCCCAAGAGAGATGGAGCTTTGATCTGC 1471
 Qy 1261 AGAGCTAATGCAAGCCCAAGATTTAGCTGTGTTAACAATGAGATCCCAATAGAA 1320
 Db 1472 AGAGCTAATGCAAGCCCAAGATTTAGCTGTGTTAACAATGAGATCCCAATAGAA 1531

Qy 1321 ATTGCCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1380
 Db 1532 ATTGCCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1591
 Qy 1381 CAAGAAAGATCAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1440
 Db 1592 CAAGAAAGATCAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1651
 Qy 1441 GCAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1500
 Db 1652 GCAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1711
 Qy 1501 CTCTACAGAGTCAATGCAAGAGCTGCTGCTTACTAGACTGTGCTTCTTGGTCTGCT 1560
 Db 1712 CTCTACAGAGTCAATGCAAGAGCTGCTGCTTACTAGACTGTGCTTCTTGGTCTGCT 1771
 Qy 1561 CTCCCAACCATGAGTGTGTTAAGAGTAAAGAGTGTCTTTCATGAAGATATTAT 1620
 Db 1772 CTCCCAACCATGAGTGTGTTAAGAGTAAAGAGTGTCTTTCATGAAGATATTAT 1831
 Qy 1621 GTTTTACATGAAATGGAATCTTGGAAATCAAGATGCTACATGATGATGTTAAAGAAAT 1680
 Db 1832 GTTTTACATGAAATGGAATCTTGG-----GAAAT 1861
 Qy 1681 CCTGTGGCCCAAAAGAGAGTACAGAACTTATAGTGTGTTCAAGAAATTAAGGG 1740
 Db 1862 CCTGTGGCCCAAAAGAGAGTACAGAACTTATAGTGTGTTCAAGAAATTAAGGG 1921
 Qy 1741 ATGGCAAGAAATGAAGTTCACTT-----ACAGCCC 1770
 Db 1922 ATGGCAAGAAATGAAGTTCACTTAAATCAAGATGCTACATGATGATGATGATGATGATGATGAT 1981
 Qy 1771 GAATATGAGTGTGCAAGAGAGAGAGTGTGTCTTGAATGCAAGTGAACATGAT 1830
 Db 1982 GAATATGAGTGTGCAAGAGAGAGAGTGTGTCTTGAATGCAAGTGAACATGAT 2041
 Qy 1831 CACACCTTATCCCTGACTGTCTGTGTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1890
 Db 2042 CACACCTTATCCCTGACTGTCTGTGTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2101
 Qy 1891 AGGTTCACTGTGTAAGAGATCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1950
 Db 2102 AGGTTCACTGTGTAAGAGATCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2161
 Qy 1951 ACCTACAGTGTGTGCAACACCACTTGGACAGAGCTGTCCGACAGAGCTGTGTGAC 2010
 Db 2162 ACCTACAGTGTGTGCAACACCACTTGGACAGAGCTGTGTCCGACAGAGCTGTGTGAC 2221
 Qy 2011 GTTGTGTGCTTCTGCAACCTGCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2070
 Db 2222 GTTGTGTGCTTCTGCAACCTGCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2281
 Qy 2071 TTGAAGTGAAGATCAATGCAAGAAAGTGTGCTGATGAGACCCAGGCGATGAC 2130
 Db 2282 TTGAAGTGAAGATCAATGCAAGAAAGTGTGCTGATGAGACCCAGGCGATGAC 2341
 Qy 2131 AACATAGCCCATTTAACAATTCATCATGCAATATGAAGATGCAATGCAAGCAGAGG 2190
 Db 2342 AACATAGCCCATTTAACAATTCATCATGCAATATGAAGATGCAATGCAAGCAGAGG 2401
 Qy 2191 CTGTGGCAACCAAGAGTGTGCAAG 2250
 Db 2402 CTGTGGCAACCAAGAGTGTGCAAG 2461
 Qy 2251 CTTTACGTGAATCTCTTCCGCTGATGAGTGAACAGATTTGGAGAGAGTGTGCC 2310
 Db 2462 CTTTACGTGAATCTCTTCCGCTGATGAGTGAACAGATTTGGAGAGAGTGTGCC 2521
 Qy 2311 AGCGAGGCTGTGAGAGATTTTGAAGAGCTGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2370
 Db 2522 AGCGAGGCTGTGAGAGATTTTGAAGAGCTGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2581

QY	2371	GTGAAAGGACTGGGATTCAGAGCCCTGATAATTGGAGAACGCTGGAAGCCCTTGAAATGT	2430
Db	2382	GTGGAAAGGACTGGGATTCAGAGCCCTGATATATTTGGATTACGTGAACCCCTTGAAATGT	2641
QY	2431	TTGCAATCTAATGGGCGCAGGCCCTTCAGTACAAAGTTAGCTGGCGCCAGAAAGATGTGAT	2490
Db	2642	TTGCAATCTAATGGGCGCAGGCCCTTCAGTACAAAGTTAGCTGGCGCCAGAAAGATGTGAT	2701
QY	2491	GATGAAATGACATCTGTGTGTGTGGCAATGTATCCAAATATATTTGTCTCAGGCAACGCCA	2550
Db	2702	GATGAAATGACATCTGTGTGTGTGGCAATGTATCCAAATATATTTGTCTCAGGCAACGCCA	2761
QY	2551	ACCTTGTTCATATCTGATCAAAAGTTAGAGCCCGAATGACATGGGGTTTGCCCCGAG	2610
Db	2762	ACCTTGTTCATATCTGATCAAAAGTTAGAGCCCGAATGACATGGGGTTTGCCCCGAG	2821
QY	2611	CCAGCTGTAGTCATGAGGACATTTCTGGAGAAACCTCCCAATGATGTGCTCCTGGGAAGCTG	2670
Db	2822	CCAGCTGTAGTCATGAGGACATTTCTGGAGAAACCTCCCAATGATGTGCTCCTGGGAAGCTG	2881
QY	2671	CGTGTGAATGTGTGAACAGTACCTTAGCCGAGGTGCACTGGGAACCAAGTACCTGTGAA	2730
Db	2882	CGTGTGAATGTGTGAACAGTACCTTAGCCGAGGTGCACTGGGAACCAAGTACCTGTGAA	2941
QY	2731	AGCATCCGAGGACACCTACAAAGGCTATGGAAATTATCTATTGGAAAGACCCAAAGTTCACT	2790
Db	2942	AGCATCCGAGGACACCTACAAAGGCTATGGAAATTATCTATTGGAAAGACCCAAAGTTCACT	3001
QY	2791	AAAAAGAAACAGACGTCACATTGAGAAAAAGATCCTCACCTTCCAAAGCAGCAAGACCTCAT	2850
Db	3002	AAAAAGAAACAGACGTCACATTGAGAAAAAGATCCTCACCTTCCAAAGCAGCAAGACCTCAT	3061
QY	2851	GGCATGTGTGCCGGGGCTTAGAGCCCTTAGCCACTACACATGTAATGTCCAGTGTCTCAT	2910
Db	3062	GGCATGTGTGCCGGGGCTTAGAGCCCTTAGCCACTACACATGTAATGTCCAGTGTCTCAT	3121
QY	2911	GGGAAAGGGGAGGGGCCCAAGCCCTACAGAGCTTATATPACTCCAGAGAGTCCCC	2970
Db	3122	GGGAAAGGGGAGGGGCCCAAGCCCTACAGAGCTTATATPACTCCAGAGAGTCCCC	3181
QY	2971	AGTGCTCCCTCGTCTTTGAAAGTTGTGTAATCCAACTGGAACCTCTCATCTTGGAAATGG	3030
Db	3182	AGTGCTCCCTCGTCTTTGAAAGTTGTGTAATCCAACTGGAACCTCTCTCATCTTGGAAATGG	3241
QY	3031	GATCCACCGAGCACCCCGAATGGCAATTTGACAGATACACCTTAAAGTATCAGCAATT	3090
Db	3242	GATCCACCGAGCACCCCGAATGGCAATTTGACAGATACACCTTAAAGTATCAGCAATT	3301
QY	3091	AACAGCACACATGATATAGGCCCTCTGTGTAATTTGAAAAATTCCTGCCAACAAACACGCG	3150
Db	3302	AACAGCACACATGATATAGGCCCTCTGTGTAATTTGAAAAATTCCTGCCAACAAACACGCG	3361
QY	3151	TGGACTTTAAAAAATTTAAATTTGACACTGCAATTAAGTTTATTTCTATGACAAACA	3210
Db	3362	TGGACTTTAAAAAATTTAAATTTGACACTGCAATTAAGTTTATTTCTATGACAAACA	3421
QY	3211	TCAGCAGATCAGGAAGTCAAAATTAACAGAGAAAGCATTAACAATGTGGATGAAGCTGTGT	3270
Db	3422	TCAGCAGATCAGGAAGTCAAAATTAACAGAGAAAGCATTAACAATGTGGATGAAGCTGTGT	3481
QY	3271	ATTCTTCCACTGATATGATGTGTGAGGCAAAAGTTCAAGCTGTAAATATCCAGATCAGCAAT	3330
Db	3482	ATTCTTCCACTGATATGATGTGTGAGGCAAAAGTTCAAGCTGTAAATATCCAGATCAGCAAT	3510
QY	3331	CTTAATGTGACAGCTGTGAGACCTATGCAATATCAGTTGGGAATATGAGGGACACAGAG	3390
Db	3511	CTTAATGTGACAGCTGTGAGACCTATGCAATATCAGTTGGGAATATGAGGGACACAGAG	3510
QY	3391	CATGTGAACCTTTATGTGAATATGTGTGACAGCAGCAACAAGAAATGAGAAAAAGAA	3450
Db	3511	CTTAATGTGACAGCTGTGAGACCTATGCAATATCAGTTGGGAATATGAGGGACACAGAG	3510
QY	3451	ATTGTAATGTGTTCTCGAGACTCTTTGGGTTAAAGGCTCTAATGCCAGAAACGACATAC	3510

Db	3511	-----	3510
QY	3511	AAAGTCGAGTGTGCTGTGGGGGACTCTGGTTTGTGAGTTGACGAGATGTGTGAG	3570
Db	3511	-----	3510
QY	3571	ACAGGCCGAGGATGGCAGGCCGAGGTGATATTGCACTCAGGGCTGTTCATTGGT	3630
Db	3511	-----AGCGATGGCAGGCCGAGGTGATATTGCACTCAGGGCTGTTCATTGGT	3562
QY	3563	CTGATGTGTGCTGTGCTCTCTTATCTTAATTTGGTGATTTGTTGCTTCATCAGAGA	3622
Db	3691	AAACAAGGTGTTAATATTCAGTTAAAGAAAGAAAGATGCCATGCGTCACTCGAATATC	3750
QY	3623	AAACAAGGTGTTAATATTCAGTTAAAGAAAGAAAGATGCCATGCGTCACTCGAATATC	3682
Db	3751	CAGCCTATGGAAGAAGATGATGGGACATTTGGAGATATACAGTGTGCAAGAACCAACAG	3810
QY	3683	CAGCCTATGGAAGAAGATGATGGGACATTTGGAGATATACAGTGTGCAAGAACCAACAG	3742
Db	3811	CCTTTGAAGAAAGGAAGTCCAACTCTTCACACAGACCTGTGAAAGAAAGATATGAGAC	3870
QY	3743	CCTTTGAAGAAAGGAAGTCCAACTCTTCACACAGACCTGTGAAAGAAAGATATGAGAC	3802
Db	3871	GACAGCCTAGTGTGACTATGAGAAAGGGGTTATGGCAGATTCATGTAGAGATGGCTCCTTT	3930
QY	3803	GACAGCCTAGTGTGACTATGAGAAAGGGGTTATGGCAGATTCATGTAGAGATGGCTCCTTT	3862
Db	3931	ATTGGACATATCAGTGTGTAAGAAAGAGAAAGGCCGCTGAAGGAAACGAAGCTCAAG	3990
QY	3863	ATTGGACATATCAGTGTGTAAGAAAGAGAAAGGCCGCTGAAGGAAACGAAGCTCAAG	3922
Db	3991	GCACCTTCTCTGTGCAAGCCATGAATTCCTTTGTTAATTTTAAAGTCAAAAGCCATA	4050
QY	3923	GCACCTTCTCTGTGCAAGCCATGAATTCCTTTGTTAATTTTAAAGTCTTTGCAATA	3982
Db	4051	TTCCATTTCTCTAGAAATGTTTATCTTAAGCTCTTGTGTCAGCCCTCTCATCTATGAA	4110
QY	3983	TTCCATTTCTCTAGAAATGTTTATCTTAAGCTCTTGTGTCAGCCCTCTCATCTATGAA	4042
Db	4111	CATATGGGTAGAGATATTTTC	4134
QY	4043	CATATGGGTAGAGATATTTTC	4066

	RESULT 4
AAV40887	ID AAV40887 standard; cDNA, 6254 BP.
XX AC	AAV40887;
XX DT	25-SEP-1998 (first entry)
XX DE	Coding sequence of clone COT72_1.
XX KM	Human; nutritional supplement; cell proliferation/differentiation; cyclokinine; immunostimulant; immunosuppressant; haematopoiesis regulator; receptor/ligand activity; cadherin/tumour invasion suppressor; anti-inflammatory; tumour inhibitor; clone COT72_1; ds.
XX OS	Homo sapiens.
XX PH	Key
FT CDS	location/Qualifiers 383..3961
FT FT	/*tag= a
FT FT	/product= "clone COT72_1"
XX FN	/note= "no stop codon given"
XX	W09824905-A2.

W09824905-A2.

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Location/Qualifiers
383. .3961
/*tag= a
/product= "clone C0722_1"
/note= "no stop codon given"
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PD 11-JUN-1998.
 XX 05-DEC-1997; 97MO-US022211.
 PF 06-DEC-1996; 96US-00762216.
 PR 03-DEC-1997; 97US-00984516.
 XX (GEMV) GENETICS INST INC.
 XX
 PI Jacobs K, Mccoy JM, Lavallie ER, Racie LA, Merberg D, Treacy M;
 PI Spaulding V, Agostino MO;
 DR MPI; 1998-333324/29.
 DR P-PSDB; AAM57900.
 XX
 PT New isolated polynucleotides encoding secreted polypeptides - isolated
 PT from a human foetal kidney cDNA library, a human adult blood cDNA library
 PT or a human adult brain cDNA library.
 XX
 PS Claim 35, Page 77-81; 109pp; English.
 CC This sequence represents the coding sequence of clone CO722_1 of the
 CC invention. This clone was isolated from a human adult brain cDNA library.
 CC The DNAs and proteins can be used as nutritional sources or supplements,
 CC or may exhibit cytokine and cell proliferation/differentiation activity,
 CC immune stimulating or suppressing activity, haematopoiesis regulating
 CC activity, receptor/ligand activity, anti-inflammatory activity,
 CC cadherin/tumour invasion suppressor activity, tumour inhibition activity
 CC or other activities
 CC
 SQ Sequence 6254 BP; 1978 A; 1274 C; 1293 G; 1704 T; 0 U; 5 Other;
 Query Match 80.2%; Score 3316; DB 2; Length 6254;
 Best Local Similarity 90.2%; Pred. No. 0;
 Matches 3758; Conservative 0; Mismatches 10; Indels 396; Gaps 4;

QY 1 CTTCAAGTTCCTCCGATGAAATTAATTAAGTTCAGACACAGCTTTCAGAAATCTT 60
 DB 269 CTTCAAGTTCCTCCGATGAAATTAATTAAGTTCAGACACAGCTTTCAGAAATCTT 328
 QY 61 TTGTGAAG 120
 DB 329 TTGTGAAG 388
 QY 121 CTTAAATTAATGCGGAG 180
 DB 389 CTTAAATTAATGCGGAG 448
 QY 181 CTGTGCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 240
 DB 449 CTGTGCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 508
 QY 241 GTTACAGCTCCACACATCAACCAACAGCTCTCAAAAGATTATTAATGACCTCCGGAG 300
 DB 509 GTTACAGCTCCACACATCAACCAACAGCTCTCAAAAGATTATTAATGACCTCCGGAG 568
 QY 301 AATATTGTAATCCAGTGTGAAGCAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
 DB 569 AATATTGTAATCCAGTGTGAAGCAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 628
 QY 361 AATGGGACATTTTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 420
 DB 629 AATGGGACATTTTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 688
 QY 421 AGCTCATTAATTAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCA 480
 DB 689 AGCTCATTAATTAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCA 748
 QY 481 TGTACAGCAAG 540
 DB 749 TGTACAGCAAG 808
 QY 541 AGATCAACATTTGTGAGCAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 600

DB 809 AGATCAACATTTGTGAGCAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 868
 QY 601 TTAGTAATTCCTCCGAG 660
 DB 869 TTAGTAATTCCTCCGAG 928
 QY 661 AATTCCTTCAAG 720
 DB 929 AATTCCTTCAAG 988
 QY 721 TATTTTCCATGCTCTCCAG 780
 DB 989 TATTTTCCATGCTCTCCAG 1048
 QY 781 AATCATCTCAACATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCA 840
 DB 1049 AATCATCTCAACATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCA 1102
 QY 841 GAATGAATGACATATAGCTGCTAATTTGAGTGAACATGAGTTTATGCTAATATCA 900
 DB 1103 -----GCTAATATCA 1111
 QY 901 AGTAG 960
 DB 1112 AGTAG 1171
 QY 961 TTAAG 1020
 DB 1172 TTAAG 1231
 QY 1021 TACTGGGCAAG 1080
 DB 1232 TACTGGGCAAG 1291
 QY 1081 AAAACCTTGACATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 1140
 DB 1292 AAAACCTTGACATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 1351
 QY 1141 AAAATGCTTGAAG 1200
 DB 1352 AAAATGCTTGAAG 1411
 QY 1201 TGGATCAG 1260
 DB 1412 TGGATCAG 1471
 QY 1261 AGAGCTAATGAG 1320
 DB 1472 AGAGCTAATGAG 1531
 QY 1321 ATTGCCCTGATGACCCAG 1380
 DB 1532 ATTGCCCTGATGACCCAG 1591
 QY 1381 CAAGAAAGATCAAG 1440
 DB 1592 CAAGAAAGATCAAG 1651
 QY 1441 GCAAAAGCATTTGTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1500
 DB 1652 GCAAAAGCATTTGTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1711
 QY 1501 GTTACCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1560
 DB 1712 GTTACCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1771
 QY 1561 GTTCCCAACATGAG 1620
 DB 1772 GTTCCCAACATGAG 1831
 QY 1621 GTTTTACATGAT 1680

Db 1832 GTTTTACATGAAATGAACTTTG-----GAAATT 1861
Qy 1681 CCTGTGCCCCAAAAGGACAGTACAGAACTTATACGTGTGGCAAGAAATTAATTAAGG 1740
Db 1862 CCTGTGCCCCAAAAGGACAGTACAGAACTTATACGTGTGTGGCAAGAAATTAATTAAGG 1921
Qy 1741 ATGGCAAGAAATGAACTTCACTT-----ACAGCCC 1770
Db 1922 ATGGCAAGAAATGAACTTCACTTAAATCAAAAGATGCTACATGATCGTTAAACAGCCC 1981
Qy 1771 GAATATGCACTGTGTGAAAAGGAGACATGTCTCTTTGAATGCAAACTGAAACCTGAT 1830
Db 1982 GAATATGCACTGTGTGAAAAGGAGACATGTGTCTTTGAATGCAAACTGAAACCTGAT 2041
Qy 1831 CACACCTTATCCCTCACTGTCTGTGGCTGAAGAACAGGGAACTGCCAGTGAATA 1890
Db 2042 CACACCTTATCCCTCACTGTCTGTGGCTGAAGAACAGGGAACTGCCAGTGAATA 2101
Qy 1891 AGGTTCACTGTGTGACAAGGATCATCTAGTGTAGCTGATGTCAGTACGATGACAGCGG 1950
Db 2102 AGGTTCACTGTGTGACAAGGATCATCTAGTGTAGCTGATGTCAGTACGATGACAGCGG 2161
Qy 1951 ACCTACAGCTGTGTGGCCAAACACCACTTGTGACAGCGTCTCGCCAGCGCTGTCTTAC 2010
Db 2162 ACCTACAGCTGTGTGGCCAAACACCACTTGTGACAGCGTCTCGCCAGCGCTGTCTTAC 2221
Qy 2011 GTTGTGTCTCTCACTCACTCACTCCAGCTCCGTTAGATGTCCCAATCCTCCCTTGAAC 2070
Db 2222 GTTGTGTCTCTCACTCACTCACTCCAGCTCCGTTAGATGTCCCAATCCTCCCTTGAAC 2281
Qy 2071 TTAGAATGACAGATCACTTGAACAAAGTGTTCAGCTGTCACTGACCCAGCGCATGAC 2130
Db 2282 TTAGAATGACAGATCACTTGAACAAAGTGTTCAGCTGTCACTGACCCAGCGCATGAC 2341
Qy 2131 AACAAATGCCCCCTTCAAAATTCATCATCTGAATATGAAATGCAATGCAACAGCCAGG 2190
Db 2342 AACAAATGCCCCCTTCAAAATTCATCATCTGAATATGAAATGCAATGCAACAGCCAGG 2401
Qy 2191 CTGTGGCAACCACTGAAGTGTCTGGAACACAGACCAAGCCAGCTGAAGCTGTCT 2250
Db 2402 CTGTGGCAACCACTGAAGTGTCTGGAACACAGACCAAGCCAGCTGAAGCTGTCT 2461
Qy 2251 CCTTACGTGAATCTCTCTCGCGTGTGTGAGAGTGAACAGCATTTGGAAAGCTTGGCC 2310
Db 2462 CCTTACGTGAATCTCTCTCGCGTGTGTGAGAGTGAACAGCATTTGGAAAGCTTGGCC 2521
Qy 2311 AGCGAGGCGTCTGACAGATATTTGACGAAGGCTCAGAACCAATATTAACCCCAACAGT 2370
Db 2522 AGCGAGGCGTCTGACAGATATTTGACGAAGGCTCAGAACCAATATTAACCCCAACAGT 2581
Qy 2371 GTGGAGAGACTGGGATCAGAGCTGATATTTGGAGATTAACGTGAAGGCTTGAATGGT 2430
Db 2582 GTGGAGAGACTGGGATCAGAGCTGATATTTGGAGATTAACGTGAAGGCTTGAATGGT 2641
Qy 2431 TTGCAATCTAATGCGCCAGGCTTCACTAATAAGTTAGCTGGCGCCAGAAAGATGTGAT 2490
Db 2642 TTGCAATCTAATGCGCCAGGCTTCACTAATAAGTTAGCTGGCGCCAGAAAGATGTGAT 2701
Qy 2491 GATGAATGACATCTGTGTGTGTGGCAATGTATCCAAATATTTGTCTCAGGACGCCA 2550
Db 2702 GATGAATGACATCTGTGTGTGTGGCAATGTATCCAAATATTTGTCTCAGGACGCCA 2761
Qy 2551 ACCTTGTTCACATCTGATCAAGTTCAGGCGCTGAATGACATGGGGTTTGGCCCCGAG 2610
Db 2762 ACCTTGTTCACATCTGATCAAGTTCAGGCGCTGAATGACATGGGGTTTGGCCCCGAG 2821
Qy 2611 CCAGCTGTAGTCACTGGGACATTTCTGAGAAAGACCTCCCAATGCTGCTCTGGGAACTGT 2670
Db 2822 CCAGCTGTAGTCACTGGGACATTTCTGAGAAAGACCTCCCAATGCTGCTCTGGGAACTGT 2881
Qy 2671 CGTGTGAATGTGTGAACAGTACCTTAGCCGAGGTGACCTGGGACCCAGTACTCTTGAA 2730
Db 2882 CGTGTGAATGTGTGAACAGTACCTTAGCCGAGGTGACCTGGGACCCAGTACTCTTGAA 2941

Qy 2731 AGCATCCGAGGACACCTTACAAAGCTATCGAATTTATCTATGGAAAGACCCAGATTCATCT 2790
Db 2942 AGCATCCGAGGACACCTTACAAAGCTATCGAATTTATCTATGGAAAGACCCAGATTCATCT 3001
Qy 2791 AAAAGAAACAGACCTGACATTTGAGAAAAGATCTTCACTTCCAGAGGACAGACTCAT 2850
Db 3002 AAAAGAAACAGACCTGACATTTGAGAAAAGATCTTCACTTCCAGAGGACAGACTCAT 3061
Qy 2851 GGCATGTTGCGGGGCTAGAGGCTTTAGGCCATCACACTGAATGTCCAGTGTCAAT 2910
Db 3062 GGCATGTTGCGGGGCTAGAGGCTTTAGGCCATCACACTGAATGTCCAGTGTCAAT 3121
Qy 2911 GGGAAAGGGAGGGGCCAGCCAGCCCTGACAGAGTCTTTAATACTCCAGAAAGATCCCC 2970
Db 3122 GGGAAAGGGAGGGGCCAGCCAGCCCTGACAGAGTCTTTAATACTCCAGAAAGATCCCC 3181
Qy 2971 AGTGTCTCCCTGCTCTTTGAAGATTTGTGAATCCAACTGTGACTCTCTCACTTTGGAATGG 3030
Db 3182 AGTGTCTCCCTGCTCTTTGAAGATTTGTGAATCCAACTGTGACTCTCTCACTTTGGAATGG 3241
Qy 3031 GATCCACGAGCCACCCGATGATGATTTGACAGAGTACACCTTAAAGTATCAGCAAT 3090
Db 3242 GATCCACGAGCCACCCGATGATGATTTGACAGAGTACACCTTAAAGTATCAGCAAT 3301
Qy 3091 AACAGCAACATGAATTAAGCCCTCTGTGATATTTGAAATTCCTGCCAACAGACAGG 3150
Db 3302 AACAGCAACATGAATTAAGCCCTCTGTGATATTTGAAATTCCTGCCAACAGACAGG 3361
Qy 3151 TGGACTTTAAATTAATTAATTTGACACTGATATTAAGTTTATTTATGACAAACA 3210
Db 3362 TGGACTTTAAATTAATTAATTTGACACTGATATTAAGTTTATTTATGACAAACA 3421
Qy 3211 TCAGCAGATCAGAAATCAATTAACAGAGAAAGATTAACAACCTGTGATGAAGTGGT 3270
Db 3422 TCAGCAGATCAGAAATCAATTAACAGAGAAAGATTAACAACCTGTGATGAAGTGGT 3481
Qy 3271 ATTCTTCCACTGATGTAGGTGACAGCAAAAGTTCAAGCTGTAATATCAAGATCAGCAAT 3330
Db 3482 ATTCTTCCACTGATGTAGGTGACAGCAAAAGTTCAAGCTGTAATATCAAGATCAGCAAA 3510
Qy 3331 CTTAAGCTGACGCTGTGAGACTATGCAATATCACTTGGGAATATGAGGACCAAG 3390
Db 3511 ----- 3510
Qy 3391 CATGTGAATTTATGTAATATGATGTGAGAGGACAGCAAAAGATGAGAAAGAA 3450
Db 3511 ----- 3510
Qy 3451 ATTGTAAATGTTCTCGAGCTTCTTTGGGTTAAAGGCTTAATGCAAGAACAGCATAC 3510
Db 3511 ----- 3510
Qy 3511 AAAGTTCAAGTTGTGTGTGGGAGACTGTGTTTGTGAGTTCAAGAGATGTGTTGAG 3570
Db 3511 ----- 3510
Qy 3571 ACAGGCCAGGATGAGCAAGCCGAGGATGATTTGCAACTCAGGGCTGTCTATTGGT 3630
Db 3511 -----AGCATGAGCAAGCCGAGGATGATTTGCAACTCAGGGCTGTCTATTGGT 3562
Qy 3631 CTGATGTGTGCTGTCTCTCTTATCTTAATTTTGTGATTTGTGCTTCAACAGAGA 3690
Db 3562 -----AGCATGAGCAAGCCGAGGATGATTTGCAACTCAGGGCTGTCTATTGGT 3622
Qy 3691 AACAAAGGTGTAAATATCACTTAAGAAAGAAAGATGCCATGTGACCTGAATC 3750
Db 3622 AACAAAGGTGTAAATATCACTTAAGAAAGAAAGATGCCATGTGACCTGAATC 3682
Qy 3751 CAGCTTATGAAGAAAGATGATGAGCACTTTGAGAAATCAAGATGACAGAAAGACCAAG 3810
Db 3683 CAGCTTATGAAGAAAGATGATGAGCACTTTGAGAAATCAAGATGACAGAAAGACCAAG 3742

QY 3811 CCTTTGAAAAAGAGTGCAGTCTCTTTCAGACAGAGCTGTGAAAAAGAGATGATGAC 3870
 DB 3743 CTTTGAAGAAAAAGAGTGCAGTCTCTTTCAGACAGAGCTGTGAAAAAGAGATGATGAC 3802
 QY 3871 GACAGCCTTACTGATCTATGAGAGAGGGGTTAATGCGCAGTTCAATGAGATGCTCTTT 3930
 DB 3803 GACAGCCTTACTGATCTATGAGAGAGGGGTTAATGCGCAGTTCAATGAGATGCTCTTT 3862
 QY 3931 ATTGGAACAATACAGTGTGTAAGAAAGAAAGACCGGCTGAAGAAACGAACCTCAGAG 3990
 DB 3863 ATTGGAACAATACAGTGTGTAAGAAAGAAAGACCGGCTGAAGAAACGAACCTCAGAG 3922
 QY 3991 GCACTCTCTCTCTGCAAGCCATGAATTCCTTTGTTAATTTTAAAGTCAAAAGCAATA 4050
 DB 3923 GCACTCTCTCTCTGCAAGCCATGAATTCCTTTGTTAATTTTAAAGTCTTTGCCAATA 3982
 QY 4051 TTCATTTCTCTGAAATGTTATCTTAAGCTCTTTGTTGTCAGCCCTCTCATACTATGAA 4110
 DB 3983 TTCATTTCTCTGAAATGTTATCTTAAGCACTGTTGTCAGCCCTCTCATACTATGAA 4042
 QY 4111 CATATGGTAGAGATATATTTTC 4134
 DB 4043 CATATGGTAGAGATATATTTTC 4066

RESULT 5
 AAF98452
 ID AAF98452 standard; cDNA; 6254 BP.
 AC AAF98452;
 XX 07-JUN-2001 (first entry)
 DT Human cDNA clone CO722_1 sequence SEQ ID 129.
 DE
 XX Human; secreted protein; nutrient; cytokine modulator; proliferation;
 KM differentiation; immune system modulator; tissue growth; chemotactic;
 KM haemostatic; thrombolytic; anti-inflammatory; tumour inhibition; ss;
 KM haematopoiesis.
 XX Homo sapiens.
 OS
 XX MO200119988-A1.
 PN 22-MAR-2001.
 PD 14-SEP-2000; 2000MO-US025135.
 PF 17-SEP-1999; 99US-00398829.
 PR (GEMT) GENETICS INST INC.
 PA Jacobo K, McCoy JM, Lavallie ER, Collins-Racie LA, Evans C;
 PI Merberg D, Treacy M, Bowman KR, Spaulding V, Agostino MJ;
 PI MPI: 2001-244801/25.
 DR P-PSDB; AAB90717.
 DR Isolated nucleic acids encoding polypeptides, useful for modulating e.g.
 PT cytokine and cell proliferation/differentiation activity, the immune
 PT system and hematopoiesis regulating activity.
 XX Claim 12; Page 456-458; 557BP; English.
 CC Human cDNA clones represented in AAF98374 - AAF98489 encode secreted
 CC proteins AAB90667 - AAB90750. The cDNA clones are isolated from various
 CC tissue types, and may be used in the prevention, treatment and diagnosis
 CC of diseases associated with inappropriate protein expression. The
 CC polypeptides and nucleic acids may be used as nutrients or to modulate
 CC cytokine and cell proliferation/differentiation activity and may also be
 CC involved in modulation of the immune system. The cDNA sequences,
 CC proteins, their agonists and/or antagonists exhibit haematopoiesis
 CC regulating activity; tissue growth activity; activin/inhibin activity;

CC chemotactic/chemokinetic activity; haemostatic and thrombolytic activity;
 CC receptor/ligand activity; anti-inflammatory activity; haematopoiesis
 CC activity; cadherin/tumour suppressor activity; and/or tumour inhibition
 CC activity. Included in the invention are probes represented in AAF98490 -
 CC AAF98572 which are specific for the cDNA clones encoding the secreted
 CC proteins
 XX

SO Sequence 6254 BP; 1978 A; 1274 C; 1293 G; 1704 T; 0 U; 5 Other;

Query Match 80.2%; Score 3316; DB 5; Length 6254;
 Best Local Similarity 90.2%; Pred. No. 0;
 Matches 3758; Conservative 0; Mismatches 10; Indels 396; Gaps 4;

QY 1 CTTCAAGTCCCGCATGAAATTAATTAAGTTGACACAGCTTTCAGAAATCTT 60
 DB 269 CTTCAAGTCCCGCATGAAATTAATTAAGTTGACACAGCTTTCAGAAATCTT 328
 QY 61 TTGTGAAG 120
 DB 329 TTGTGAAG 388
 QY 121 CTTAAATATATGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
 DB 389 CTTAAATATATGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 448
 QY 181 CTGTGCAAGATGATTAGTCACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
 DB 449 CTGTGCAAGATGATTAGTCACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 508
 QY 241 GTACAGCCTCCACAGATCAACCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
 DB 509 GTACAGCCTCCACAGATCAACCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 568
 QY 301 AATATTGTTATCAAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
 DB 569 AATATTGTTATCAAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 628
 QY 361 AATGGAGATCAATTTGAGATGATGATGATGATGATGATGATGATGATGATGAT 420
 DB 629 AATGGAGATCAATTTGAGATGATGATGATGATGATGATGATGATGATGATGAT 688
 QY 421 ACGCTCATTAATTAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCA 480
 DB 689 ACGCTCATTAATTAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCA 748
 QY 481 TGTACAG 540
 DB 749 TGTACAG 808
 QY 541 AATACACCATTTGAG 600
 DB 809 AATACACCATTTGAG 868
 QY 601 TTAGTACTTCCCTGAG 660
 DB 869 TTAGTACTTCCCTGAG 928
 QY 661 AATTCCTTTCAAG 720
 DB 929 AATTCCTTTCAAG 988
 QY 721 TATTTTTCAGATGCTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
 DB 989 TATTTTTCAGATGCTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1048
 QY 781 AATCACTACCAACATACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
 DB 1049 AATCACTACCAACATACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1102
 QY 841 GAATGAATGACATATAGCTGCTAATTTGAGTGAAGTGAAGTGAAGTGAAGTGAAG 900
 DB 1103 -----GCTAAATCA 1111

Qy	901	GGTGAAGAGAGAGCCCAACACTTTTAACTCACAAGGCAATGCAAGTAAACAAGAGAA	960
Db	1112	AGTAGAGAGAGCCCAACAACTTTTAACTCACAAGGCAATGCAAGTAAACAAGAGAA	1171
Qy	961	TTAAGAGAAATGAGCTTTCATCTGAGAGCATTTGCAGAAAGCACTGCTACCCCAATTAT	1020
Db	1172	TTTAAGAGAAATGAGCTTTCATCTGAGAGCATTTGCAGAAAGCACTGCTACCCCAATTAT	1231
Qy	1021	TACTGGGCAAGAAAGATGGAATGCTACCCAAAACAGACAGTTTATAGAACTTTGAG	1080
Db	1232	TACTGGGCAAGAAAGATGGAATGCTACCCAAAACAGACAGTTTATAGAACTTTGAG	1291
Qy	1081	AAAACCTTGCAATCATTCATGTTTACAAGACAGACTGTGAAATTTACAAATGATAGCA	1140
Db	1292	AAAACCTTGCAATCATTCATGTTTACAAGACAGACTGTGAAATTTACAAATGATAGCA	1351
Qy	1141	AAAAATGATTAGAGAGCCATCCACCATATTCATTTCTGTTAGATTAAAGCGGCTCATAC	1200
Db	1352	AAAAATGATTAGAGAGCCATCCACCATATTCATTTCTGTTAGATTAAAGCGGCTCATAC	1411
Qy	1201	TGATCACAAGCCCTCAAAATCTTGTGCTGTCCCAAGAGAGATGGGACTTGAATCTGC	1260
Db	1412	TGATCACAAGCCCTCAAAATCTTGTGCTGTCCCAAGAGAGATGGGACTTGAATCTGC	1471
Qy	1261	AGAGCTATGCGAACCCCAACCCAGATTAAGCTGTAAACAATGGAGTCCCAATAGAA	1320
Db	1472	AGAGCTATGCGAACCCCAACCCAGATTAAGCTGTAAACAATGGAGTCCCAATAGAA	1531
Qy	1321	ATTGCCCCGTATGACCCCGACAGAAATATAGTGGCGATACCATATATTTTTCAAATGTT	1380
Db	1532	ATTGCCCCGTATGACCCCGACAGAAATATAGTGGCGATACCATATATTTTTCAAATGTT	1591
Qy	1381	CAAGAAAGATCAAGTGCAGTATATCATGTCAATGCTCTTAATGAATATGATATTACTG	1440
Db	1592	CAAGAAAGATCAAGTGCAGTATATCATGTCAATGCTCTTAATGAATATGATATTACTG	1651
Qy	1441	GCAAAAGCATTTGTAAATATGCTGCTGACGACACACGAATCTCAACCTCGACAAACACA	1500
Db	1652	GCAAAAGCATTTGTAAATATGCTGCTGACGACACACGAATCTCAACCTCGACAAACACA	1711
Qy	1501	CTCTACCAAGTCATGTCAAACAGGCGCTCTTATACAGCTGCGCTTCTTGGGCTCTCT	1560
Db	1712	CTCTACCAAGTCATGTCAAACAGGCGCTCTTATACAGCTGCGCTTCTTGGGCTCTCT	1771
Qy	1561	CTCCCAACCATGAGTGTGTTTAAAGAGCTTAAAGAGTGTCTTTCATGAAGATATTTAT	1620
Db	1772	CTCCCAACCATGAGTGTGTTTAAAGAGCTTAAAGAGTGTCTTTCATGAAGATATTTAT	1831
Qy	1621	GTTTTCACATGAAATATGAACTTTGGAATTCAAAGATGCTACATGGAATGTTAAAGAAAT	1680
Db	1832	GTTTTCACATGAAATATGAACTTTG---GAAAT	1861
Qy	1681	CCTGTGGCCCAAAAGAGACAGTACAGAACTTATACGTGTGTTGCAAGATAAATTAAGG	1740
Db	1862	CCTGTGGCCCAAAAGAGACAGTACAGAACTTATACGTGTGTTGCAAGATAAATTAAGG	1921
Qy	1741	ATGGCAAAAGATGAAGTTCATT-----ACAGCC	1770
Db	1922	ATGGCAAAAGATGAAGTTCATTAAATCAAAAGATGCTACATGGAATGTTAAACAGCC	1981
Qy	1771	GAAATATGCAATGTGCAAAAGAGGAGCATGTGTCTTGAATGCAAGTAAACATGAT	1830
Db	1982	GAAATATGCAATGTGCAAAAGAGGAGCATGTGTCTTGAATGCAAGTAAACATGAT	2041
Qy	1831	CACACCTTATCCCTCACTGCTCTGTGGCTGAAGAGCAACAGGAACTGCCAGATGATA	1890
Db	2042	CACACCTTATCCCTCACTGCTCTGTGGCTGAAGAGCAACAGGAACTGCCAGATGATA	2101
Qy	1891	AGGTTCACTGTGACAAAGATCATATGATGTAGCTGATGTCAATGACATGACACGCGG	1950
Db	2102	AGGTTCACTGTGACAAAGATCATATGATGTAGCTGATGTCAATGACATGACACGCGG	2161
Qy	1951	ACCTACAGGTGTGGCCACACCACTCTGACAGCGTCTCGCCAGCGCTGTGTAC	2010

Db	2162	ACCTAACCGTGTGGCCAAACCAACTCTGACAGGGCTCTCCGCAGCGCTGTGCTTAGC	2221
OY	2011	GTTGTTGCTCTTACTCCAACTCCAGCTCCCGTTTAGATGTGCCCAATCTCTCCCTTTGAC	2070
Db	2222	GTTGTGTCTCTTACTCCAACTCCAGCTCCCGTTTAGATGTGCCCAATCTCTCTTTTGAC	2281
OY	2071	TTTGAACCTGACAGATCAACTTTGACAAAAGTTCAGGTGTCAATGACCCCGAGCGATGAC	2130
Db	2282	TTTGAACCTGACAGATCAACTTTGACAAAAGTTCAGGTGTCAATGACCCCGAGCGATGAC	2341
OY	2131	AACAAATAGCCCAATTACAAATTCATCATCGAATATGAGATGCATGCAACAAGCCAGGG	2190
Db	2342	AACAAATAGCCCAATTACAAATTCATCATCGAATATGAGATGCATGCAACAAGCCAGGG	2401
OY	2191	CTGTGGGACCAACCAACTGAAAGTTTCTGGAAACAAGACCAAGCCGACGTGAAGCTGTCT	2250
Db	2402	CTGTGGGACCAACCAACTGAAAGTTTCTGGAAACAAGACCAAGCCGACGTGAAGCTGTCT	2461
OY	2251	CCTTAAGTGAACACTCTCTTCCGGGTATAGGACAGTGAACAGCAATTTGGGAAGAGCTTGCC	2310
Db	2462	CCTTAAGTGAACACTCTCTTCCGGGTATAGGACAGTGAACAGCAATTTGGGAAGAGCTTGCC	2521
OY	2311	AGCGAGCGCTCTGAGCAGTATTTGACCGAAAGCCTCAGAACAGATAAAAAACCCACAGCT	2370
Db	2522	AGCGAGCGCTCTGAGCAGTATTTGACCGAAAGCCTCAGAACAGATAAAAAACCCACAGCT	2581
OY	2371	GTTGGAAGGACTGGGATCAGAGCCTGTGAATTTTGGAGATTACGTGGAAAGCCCTTGAATGCT	2430
Db	2582	GTTGGAAGGACTGGGATCAGAGCCTGTGAATTTTGGAGATTACGTGGAAAGCCCTTGAATGCT	2641
OY	2431	TTTGAATCTAATGGGGCCAGGCGCTTCACTACAAAGTTAGCTGGGGCCGAGAAAGATGGTAT	2490
Db	2642	TTTGAATCTAATGGGGCCAGGCGCTTCACTACAAAGTTAGCTGGGGCCGAGAAAGATGGTAT	2701
OY	2491	GATGAATGGAACATCTGTGTGTGTGGCAAAATGTATCCAAATATATTTGTCTCAGCACGCCA	2550
Db	2702	GATGAATGGAACATCTGTGTGTGTGGCAAAATGTATCCAAATATATTTGTCTCAGCACGCCA	2761
OY	2551	ACCTTTGTTCCATTACTGATTCAAAAGTTCCAGGCCCTGAATGACATGGGGTTTGCCCCCGAG	2610
Db	2762	ACCTTTGTTCCATTACTGATTCAAAAGTTCCAGGCCCTGAATGACATGGGGTTTGCCCCCGAG	2821
OY	2611	CCAGCTGTAGTCATGGGACCAATTCGAGGAAGACCTCCCAATGGTGGCTCCCTGGGAAAGTGT	2670
Db	2822	CCAGCTGTAGTCATGGGACCAATTCGAGGAAGACCTCCCAATGGTGGCTCCCTGGGAAAGTGT	2881
OY	2671	CGTGTGATGTGTGTGAACAGTAACTTTAGCCGAGGTGCACTGGGACCCAGTAACTCTGAAA	2730
Db	2882	CGTGTGATGTGTGTGAACAGTAACTTTAGCCGAGGTGCACTGGGACCCAGTAACTCTGAAA	2941
OY	2731	AGCATCCGAGGACACTTACAAAGGCTATTCGATTTACTATTGGAAAGCCAGAGTTCACTCT	2790
Db	2942	AGCATCCGAGGACACTTACAAAGGCTATTCGATTTACTATTGGAAAGCCAGAGTTCACTCT	3001
OY	2791	AAAAAGAAACAGAGTCACATTGAAAAAAGATCTCTCACTTTCAAAGGACGAAACATCAT	2850
Db	3002	AAAAAGAAACAGAGTCACATTGAAAAAAGATCTCTCACTTTCAAAGGACGAAACATCAT	3061
OY	2851	GGCATGTGTGCGGGGCTTAGAGCCCTTTTAGCCATCACTAGATGTCTCGAGTGGTCAAT	2910
Db	3062	GGCATGTGTGCGGGGCTTAGAGCCCTTTTAGCCATCACTAGATGTCTCGAGTGGTCAAT	3121
OY	2911	GGGAAAGGGAGGGGCCAGCCAGCCCTTGACAGAGTCTTTTAATCTCCAGAAAGAGTCCCC	2970
Db	3122	GGGAAAGGGAGGGGCCAGCCAGCCCTTGACAGAGTCTTTTAATCTCCAGAAAGAGTCCCC	3181
OY	2971	AGTGTCTCCTCTGTCTTTGAAGATTGTGAAATCCAACTAGGACTCTCTCACTTTGGAAATGG	3030
Db	3182	AGTGTCTCCTCTGTCTTTGAAGATTGTGAAATCCAACTAGGACTCTCTCACTTTGGAAATGG	3241
OY	3031	GATCACCGAGCCACCGGAATGGCAATTTTGAAGATTAACACTTAAGATACAGCAATT	3090

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Db 3242 GATCCAGCCGAGCCAGCCGATTTTGAAGAGTACCTTAAGTATGACCAATT 3301
Qy 3091 AACAGCACATGATTAATAGAGCCCTCTGTAGATTTGAAATTCCTGCCAACAAGACGG 3150
Db 3302 AACAGCACATGATTAATAGAGCCCTCTGTAGATTTGAAATTCCTGCCAACAAGACGG 3361
Qy 3151 TGGACCTTTAAATAATTTAAATTTAGCACTGATATTAAGTTTATTTCTATGCAACAACA 3210
Db 3362 TCGACCTTTAAATAATTTAAATTTAGCACTGATATTAAGTTTATTTCTATGCAACAACA 3421
Qy 3211 TACAGCAGATTCAGAAAGTCAATTAACAGAGAAAGCACTGTAACAATGATAGTGGT 3270
Db 3422 TCAGAGAGATTCAGAAAGTCAATTAACAGAGAAAGCACTGTAACAATGATAGTGGT 3481
Qy 3271 ATTCTTCCACTGATGATGAGGCAAAAGTTCAAGCTGTAATAATACAGATCAGCAAT 3330
Db 3482 ATTTCTTCCACTGATGATGAGGCAAAAGTTCAAGCTGTAATAATACAGATCAGCAAT 3510
Qy 3331 CTTAAGTTCAGAGCTGCTGAGACCTATGCAATATCATGTTGGGAATATGAGGACACAG 3390
Db 3511 ----- 3510
Qy 3391 CATGTGAACCTTTAATGTTGAATATGTTGATGACAGCAGCAAGAAAGATGAGAAAACA 3450
Db 3511 ----- 3510
Qy 3451 ATTGTAATGTTCTTCGAGCTTCTTTGGGTTAAAGGCTTAATGCGAGAAACAGATAC 3510
Db 3511 ----- 3510
Qy 3511 AAAAGTTCAGATTGCTGTGGGGAATCTGTGTTTGTGATTCAGAGAGTGTGTTGAG 3570
Db 3511 ----- 3510
Qy 3571 ACAGGCCAGCAGTGGCAAGCCGCGAGGTGATTAATGCACTCAGGCGTGTTCATTGGT 3630
Db 3511 ----- 3510
Qy 3511 ----- 3510
Qy 3631 CTGATGTCGTCGTCCTCTCTTAAATTTTGTGATGTTGCTGCTCATGAGAA 3690
Db 3511 ----- 3510
Qy 3631 CTGATGTCGTCGTCCTCTCTTAAATTTTGTGATGTTGCTGCTCATGAGAA 3690
Db 3631 CTGATGTCGTCGTCCTCTCTTAAATTTTGTGATGTTGCTGCTCATGAGAA 3690
Qy 3691 AACAGGGGTGTAATATCAGTAAAGAAAGAAAGTCCCATGCTGACCTGAAATC 3750
Db 3631 AACAGGGGTGTAATATCAGTAAAGAAAGAAAGTCCCATGCTGACCTGAAATC 3682
Qy 3751 CAGCCTATGAAGAGATGATGAGCAATTTGAGAAATACATGATGACAGAAACCAAG 3810
Db 3682 CAGCCTATGAAGAGATGATGAGCAATTTGAGAAATACATGATGACAGAAACCAAG 3742
Qy 3811 CTTTGAAGAAAGAAAGTGAATCTCTTCAGACAGATCTGTAAGAAAGAAAGTATGAC 3870
Db 3742 CTTTGAAGAAAGAAAGTGAATCTCTTCAGACAGATCTGTAAGAAAGAAAGTATGAC 3802
Qy 3871 GACAGCCTATGATGATGAGAAAGGGGTTAATGAGCAATGATGATGATGATGATGAT 3930
Db 3802 GACAGCCTATGATGATGAGAAAGGGGTTAATGAGCAATGATGATGATGATGATGATGAT 3862
Qy 3931 ATTGACAAATACATGATGAGAAAGAAAGAAAGGCGGCTGAGAAAGCAAGTCTCAGAG 3990
Db 3862 ATTGACAAATACATGATGAGAAAGAAAGAAAGGCGGCTGAGAAAGCAAGTCTCAGAG 3922
Qy 3991 GCACTTCTCTGTAAGGCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4050
Db 3922 GCACTTCTCTGTAAGGCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3982
Qy 4051 TTCCATTTCTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4110
Db 3982 TTCCATTTCTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4042
Qy 4111 CATATGGGTAGAGATATTTTC 4134
Db 4042 CATATGGGTAGAGATATTTTC 4066

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RESULT 6
ADE77114/C
ID ADE77114 standard; cDNA, 6384 BP.
XX
XX ADE77114;
AC ADE77114;
XX
XX 29-JAN-2004 (first entry)
DT
XX
DE Human cDNA differentially expressed in a liver disorder #206.
XX
XX human; ss; gene; liver disorder; hyperlipidemia; hypertension;
XX type II diabetes; tumour; liver; inflammatory disorder;
XX immune response disorder; high-throughput screening;
XX differential gene expression; gene therapy.
XX
OS Homo sapiens.
XX
XX US2003108871-A1.
XX
XX 12-JUN-2003.
XX
XX 30-JUL-2001; 2001US-00919039.
XX
XX 28-JUL-2000; 2000US-0222113P.
XX
XX (KASER) KASER M R.
XX
XX Kaser MR;
XX
XX WPI, 2004-031227/03.
XX
XX Composition comprising several cDNAs that are differentially expressed in
XX treated human C3A liver cell cultures, useful for treating liver
XX disorders.
XX
XX Claim 1; SEQ ID NO 279; 41pp; English.
XX
XX The invention relates to a composition comprising several cDNAs that are
XX differentially expressed in a liver disorder. The composition is useful
XX for treating liver disorder such as hyperlipidemia, hypertension, type
XX II diabetes, tumours of the liver and disorders of the inflammatory and
XX immune response. The composition is useful for a high-throughput method
XX of screening several molecules or compounds to identify a ligand which
XX specifically binds a cDNA. A protein encoded by the cDNA is useful for a
XX high-throughput method for using a protein to screen several molecules or
XX compounds to identify at least one ligand which specifically binds the
XX protein which involves combining the protein encoded by the cDNA with
XX several of molecules or compounds under conditions to allow specific
XX binding, and detecting specific binding between the protein and a
XX molecule or compound, therefore identifying a ligand which specifically
XX binds the protein. The composition is useful for detecting and
XX quantifying differential gene expression, can be used in gene therapy, to
XX formulate prognosis and to design a treatment regimen and to monitor the
XX efficacy of treatment. The present sequence represents a cDNA
XX differentially expressed in a liver disorder.
XX
XX Sequence 6384 BP; 1718 A; 1375 C; 1328 G; 1963 T; 0 U; 0 Other;
SQ
Query Match 78.2%; Score 3233.6; DB 10; Length 6384;
Best Local Similarity 89.4%; Pred. No. 0;
Matches 3722; Conservative 0; Mismatches 9; Indels 433; Gaps 5;
Qy 1 CTTGAAGTTCCTCCGATGAAATTAATTAACCTTGACACAAAGTTTCAGAAATCTT 60
Db 5927 CTTGAAGTTCCTCCGATGAAATTAATTAACCTTGACACAAAGTTTCAGAAATCTT 5869
Qy 61 TTGGAAGAAAGAAAGAAATTCAGTGTGATCTCAGAGAGTAAAGCTAATCAG 120
Db 5868 TTGGAAGAAAGAAAGAAATTCAGTGTGATCTCAGAGAGTAAAGCTAATCAG 5809
Qy 121 CTTAAATATATGCGAAAGAAAGCGCTTAATCTCGGAGAGAGTCCCTGATTTCTCTTC 180

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QY 2311 AGGAGGCGCTGAGAGATTTTGAAGAAAGCTCAGAAACAGATATAAAACCCACAGCT 2370
 DB 3675 AGGAGGCGCTGAGAGATTTTGAAGAAAGCTCAGAAACAGATATAAAACCCACAGCT 3616
 QY 2371 GTGGAAGAAGCTGGATCAGAGCTGATTAATTGGAGATTACGTGAAGCCCTTTGAATGCT 2430
 DB 3615 GTGGAAGAAGCTGGATCAGAGCTGATTAATTGGAGATTACGTGAAGCCCTTTGAATGCT 3556
 QY 2431 TTGGAATCTAATGAGGCGAGGCTTCAGTACAAAGTTAGCTGGGCGCAAGAAAGTGTGAT 2490
 DB 3555 TTGGAATCTAATGAGGCGAGGCTTCAGTACAAAGTTAGCTGGGCGCAAGAAAGTGTGAT 3496
 QY 2491 GATGAATGAGCAATCTGAGTGTGGAATGTATCCAAATATATGCTCAGGACAGCA 2550
 DB 3495 GATGAATGAGCAATCTGAGTGTGGAATGTATCCAAATATATGCTCAGGACAGCA 3436
 QY 2551 ACCTTTGTTCCATACCTGATCAAAAGTTCAGGCCCTGAATGACATGGGGTTTGCCTCCGAG 2610
 DB 3435 ACCTTTGTTCCATACCTGATCAAAAGTTCAGGCCCTGAATGACATGGGGTTTGCCTCCGAG 3376
 QY 2611 CCAGCTGTAGTCAATGGGACATTTCTGGAAGAACTCCCAATGTGCTCTGGGAACGTG 2670
 DB 3375 CCAGCTGTAGTCAATGGGACATTTCTGGAAGAACTCCCAATGTGCTCTGGGAACGTG 3316
 QY 2671 CGTGTGAATGTGGTGAACAGTACCTTAGCCGAGGTGACATGGGACCCAGTACCTTGAA 2730
 DB 3315 CGTGTGAATGTGGTGAACAGTACCTTAGCCGAGGTGACATGGGACCCAGTACCTTGAA 3256
 QY 2731 AGCATCCAGAGCACCTACACAGGCTATCGGATTTACTATTGGAAGACCAAGATTCATCT 2790
 DB 3255 AGCATCCAGAGCACCTACACAGGCTATCGGATTTACTATTGGAAGACCAAGATTCATCT 3196
 QY 2791 AAAAGAAACAGAGCTCACTTGAAGAAAGATCTCTCACTTCCAAAGCAGCAAGATCTCAT 2850
 DB 3195 AAAAGAAACAGAGCTCACTTGAAGAAAGATCTCTCACTTCCAAAGCAGCAAGATCTCAT 3136
 QY 2851 GGCATTTGCGGGGGCTAGAGCCCTTTAGCACTACACAGTAACTCCGAGTGCAT 2910
 DB 3135 GGCATTTGCGGGGGCTAGAGCCCTTTAGCACTACACAGTAACTCCGAGTGCAT 3076
 QY 2911 GGGAAAGGGGAGGGCCAGCAGCCCTGACAGAGTCTTTAATATCTCCAGAAAGAGTCCCC 2970
 DB 3075 GGGAAAGGGGAGGGCCAGCAGCCCTGACAGAGTCTTTAATATCTCCAGAAAGAGTCCCC 3016
 QY 2971 AGTGTCTCCTCGTCTTTGAAGATTGGAATCCAACTGGAATCTCTCACTTTGGAATG 3030
 DB 3015 AGTGTCTCCTCGTCTTTGAAGATTGGAATCCAACTGGAATCTCTCACTTTGGAATG 2956
 QY 3031 GATCCACGAGCCAGCCGAGTGGCATTTTGAAGAGTACACCTTAAGATTCAGCAAT 3090
 DB 2955 GATCCACGAGCCAGCCGAGTGGCATTTTGAAGAGTACACCTTAAGATTCAGCAAT 2896
 QY 3091 AACAGACACATGAATTAAGCCCTCTGTAGATTTTGAATTTCTGCCAAACAGACAGCG 3150
 DB 2895 AACAGACACATGAATTAAGCCCTCTGTAGATTTTGAATTTCTGCCAAACAGACAGCG 2836
 QY 3151 TGGACTTTAAAAATTTAAATTTTCAAGCTCGATGATTAATTTTCTATGCAAAACA 3210
 DB 2835 TGGACTTTAAAAATTTAAATTTTCAAGCTCGATGATTAATTTTCTATGCAAAACA 2776
 QY 3211 TCAGCAGGATCCAGAGTCAAAATTAAGAGAAAGCACTGATGATGAGTGTGAT 3270
 DB 2775 TCAGCAGGATCCAGAGTCAAAATTAAGAGAAAGCACTGATGATGAGTGTGAT 2723
 QY 3271 ATCTTCCACCTGATGTAGGTGACAGCAAAAGTTCAGCTGTAAATCCAGATCAGCAAT 3330
 DB 2722 ATCTTCCACCTGATGTAGGTGACAGCAAAAGTTCAGCTGTAAATCCAGATCAGCAAT 2723
 QY 3331 CTTACTGTGACGTGCTGAGACCTATGCCAATATACGTTGGAAATATGAGGACCAAG 3390
 DB 2722 CTTACTGTGACGTGCTGAGACCTATGCCAATATACGTTGGAAATATGAGGACCAAG 2723

QY 3391 CATGTGAACCTTTAATGTTGAATATGTTGTAGAGCGACAGCAAGAAAGAAATGAGAAAGAA 3450
 DB 2722 CATGTGAACCTTTAATGTTGAATATGTTGTAGAGCGACAGCAAGAAAGAAATGAGAAAGAA 2723
 QY 3451 ATTGTAAATGTTCTCGAGACTTCTTTGGGTTAAAGGGCTTAATGCCAGAAACAGCATAC 3510
 DB 2722 ATTGTAAATGTTCTCGAGACTTCTTTGGGTTAAAGGGCTTAATGCCAGAAACAGCATAC 2723
 QY 3511 AAAAGTTGAGTTGATGTGTGGGAGACTGTGGTTTGTGATTTAGAGGATGTGTTGAG 3570
 DB 2722 AAAAGTTGAGTTGATGTGTGGGAGACTGTGGTTTGTGATTTAGAGGATGTGTTGAG 2723
 QY 3571 ACAGGCCAGCGATGAGCAAGCCGAGAGTGAATATTGCAACTCAGAGCTGTTCATGCT 3630
 DB 2722 ACAGGCCAGCGATGAGCAAGCCGAGAGTGAATATTGCAACTCAGAGCTGTTCATGCT 2671
 QY 3631 CTGATGTGTGCTGTGCTCTCTCTTAATTTTGAATTTGCTGATTTGCTTCTTCAAGAGA 3690
 DB 2670 CTGATGTGTGCTGTGCTCTCTCTTAATTTTGAATTTGCTGATTTGCTTCTTCAAGAGA 2611
 QY 3691 AACAAAGGTTGTAATATCCAGTTAAAGAAAGAAAGTGCATGCTGACCCCTGAATATC 3750
 DB 2610 AACAAAGGTTGTAATATCCAGTTAAAGAAAGAAAGTGCATGCTGACCCCTGAATATC 2551
 QY 3751 CAGCCTATGAGAAAGATGATGAGCAATTTGGAAGATACAGTATGCAAGAACCAAG 3810
 DB 2550 CAGCCTATGAGAAAGATGATGAGCAATTTGGAAGATACAGTATGCAAGAACCAAG 2491
 QY 3811 CTTTGAAGAAAGAAAGTGCATCTCCTTCAAGAGCTGTGAAGAAAGAAAGATGTGAC 3870
 DB 2490 CTTTGAAGAAAGAAAGTGCATCTCCTTCAAGAGCTGTGAAGAAAGAAAGATGTGAC 2431
 QY 3871 GACAGCTAGTTGATGATGAGAAAGGGTTAATGSCAGTTCAATGAGAGTGCCTT 3930
 DB 2430 GACAGCTAGTTGATGATGAGAAAGGGTTAATGSCAGTTCAATGAGAGTGCCTT 2371
 QY 3931 ATTGACAAATACAGTGTGAAGAAAGAAAGAAAGCCGCTGAGAAAGAAAGTCCAG 3990
 DB 2370 ATTGACAAATACAGTGTGAAGAAAGAAAGAAAGCCGCTGAGAAAGAAAGTCCAG 2311
 QY 3991 GCACTTCTCCTGTGCAAGCCATGAATCTTTGTTAATTTTAAAGCTCAAAAGCAATA 4050
 DB 2310 GCACTTCTCCTGTGCAAGCCATGAATCTTTGTTAATTTTAAAGCTCAAAAGCAATA 2251
 QY 4051 TTCCATTTCTCAGAGTGTATCTTAAGCTCTTGTGCAAGCCCTCATATATGA 4110
 DB 2250 TTCCATTTCTCAGAGTGTATCTTAAGCACTTGTGTGCAAGCCCTCATATATGA 2191
 QY 4111 CATATGGGTAGAGATATATTTTC 4134
 DB 2190 CATATGGGTAGAGATATATTTTC 2167

RESULT 7
 AAS16294
 ID AAS16294 strand: cdna; 3943 BP.
 XX AAS16294;
 AC
 AC
 DT 14-FEB-2002 (first entry)
 XX
 DE CDNA encoding chicken Nr-CAM.
 XX Neurite outgrowth; fibronectin Type III repeat; cell adhesion molecule;
 KW F80; Fn3-5; Fn4-5; neurone; peripheral nerve damage; trauma; infarction;
 KW degenerative disease; malignant disease; antibacterial;
 KW central nervous system lesion; virucide; antiparkinsonian; nootropic;
 KW gliosis; neuroprotective; antiinflammatory; chicken; Nr-CAM; ss.
 XX
 OS Gallus sp.
 XX
 XX
 Key Location/Qualifiers
 CDS 33..3839
 FT

1384 ACTGCTTATTTTGGTCACTTAAGCCTGAAATCGAATGTTTAGGGAGTGAAGATA 1443
1598 GTGCTCTTATGAAGATTTATTTATTTTCAATGAATAATGAACTTTGAAATGAAGATG 1657
1444 GCACTTGGAGGAATTAATATGTTTTCATATATATGAACTTTGAAATATTCAGTGG 1503
1658 CTACATGATCTTTAAAGAAATTCCTGTGGCCCAAGACAGTACAGAACTTATACGT 1717
1504 CTCAGAAAGTATGTACTGGCACTATACATGTTTCAAGAGATTAATTAAGGAACACG 1563
1718 GTGTTGAAAGAAATTAATTTGAGATGGCAAGATGAAGTTCACTTACAGCCCAATG 1777
1564 AAATGAAGTACCACTGAAGTTAAAGACCAACGATGAATTAATTAACAGCCCACTGA 1623
1778 CAGTTTGCAAGAGGAGAGATGTTCTTTGAATGCAAGGAATGAATGACACCT 1837
1624 AAGTGAATCAAGATCTGCCAGGCTTCATTGATGTTGAATTAATTAACATGATCTTAC 1683
1838 TATCCCTCACTGCTGTGGCTGAAGACAAACAGGAACTGCCAGTGAATGAAGTTCA 1897
1684 TATATCAACAGTATATATGCTGAAGACAAATATGATACCAAGATGATGAAGTTTC 1743
1898 CTGTTGACAGAGATCACTAGTGTAGCTGATGTCACTGACATGACAGCGGAGCTTACA 1957
1744 TGTGTGTAAGAACACTTGACCATTAATGATTAATGATTAAGATGAATGAACATATA 1803
1958 CGTGTGTGGCCACACCACTGTGACAGGCTCTCCCGAGGCTGTAGGCTTGAAGTTG 2017
1804 CTTGCAATGTTAAATCTACTCTGACAGTGTTCACAGAGTCTGTGCTTACTGTGTTG 1863
2018 CTCTCACTCAACTCCAGCTCCGTTTACGATGTCCCAATCTCTCTTTGACTTGAAC 2077
1864 CTGCTCCCAATCTCCAGCTATATTTACCTCGGCAATTCACCGCTTGAATTTGAAAT 1923
2078 TGAAGATCAACTGACAAAGTGTCACTGTATGATGAACCCAGCGATGACACACATA 2137
1924 TGAAGATCACTGACAAAGTGTCACTGTATGATGAACCCAGCGATGACACACATA 1983
2138 GCGCCATTACAAATTCATCATTTGAAATTTGAAGATGCAATGCAAGCCAGGCTGTGG 2197
1984 GTCCCACTTACAACTTTGATTTGAGATGAAATGACATGACATGACCGAGGATGAC 2043
2198 ACCCAAACTGAAGTTCTGAAACACAGACCAAGCCAGCTGAGCTGTCTCTTACG 2257
2044 ATTACAGAGGAATTCCTGATCTCATACATGATGATGATGATGATGATGATGATG 2103
2258 TGAATCTCTCTTCCGCTGATGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 2317
2104 TCACTACTCATCTCCGTGATGCTGTCAATGAATTTGATGAAGTCAAGCAAGTGAAC 2163
2318 CGTCTGAGATTTTGAAGAAAGCTCAGAACCAATTAATTAATTAATTAATTAATTAAT 2377
2164 CATCTGAAGATCTGACAAAGTCCGCAAACTCCATGAAATCTTTTAAATGAACAG 2223
2378 GACTGGATCAAGACCTGATTAATTTGAGATTTAGTGAAGCTTTGAATGTTTGAAT 2437
2224 GATGAGCTCGAAGCTGATTAATTTGATTAATGATGATGATGATGATGATGATGAT 2283
2438 CTAAATGGGCAAGGCTTCACTGATCAAAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 2497
2284 CTAAATGGGCAAGGCTTCACTGATTAATTTGATGATGATGATGATGATGATGATG 2343
2498 GATGATCTGT 2557
2344 GAGAGCTGT 2403
2558 TTTCCATCACTGATCAAGTTCAGGCTGATGATGATGATGATGATGATGATGATGATG 2617
2404 TTTCCATCACTGATCAAGTTCAGGCTGATGATGATGATGATGATGATGATGATGATG 2463
2618 TATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2677
2464 AGGTATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2523

2678 ATGTGATGAACAGTACCTTACGAGTGCATCTGGGACCCAGTACCTTGAAGAGATCC 2737
2524 ATGTATTTAAGACATTTGGAAAGTGCATCTGGGACCCAGTACCTTGAAGAGATCC 2583
2738 GAGACACCTACAGGCTATCGAATTTATCTATTTGAAGACCAAGTTCATTTAAAGAA 2797
2584 GAGACATCTTCAAGATTAATTAAGTGTACTGGAAGATGATGATGATGATGATGATG 2643
2798 AAGAGCTCACATTTGAAGAAAGATCTCAGCTTCCAGGAGCAAGATCTGATGATG 2857
2644 GTAAACGGATGATGAAGAAAGATCTGATCTTGAAGGAAAGCAAGATTTTGAAGAT 2703
2858 TCCCGGGGCTAGAGCTTTTACCACTGACATGATGTCGAGTGTCAATGGAAGAA 2917
2704 TACAGAGGCTAGAGCTTATGATTTTCAAGCTGATGATGATGATGATGATGATG 2763
2918 GAGAGGGGCCAGCCAGCCCTGACAGATCTTTAATATCTCAGAGAGATCCCAAGTCT 2977
2764 GAGAGGACCAAGCAAGCCAGCAAGATTTAAATCTCTGAAGAGATCTTACGCCAC 2823
2978 CTTCTCTTTGAAGATTTGATTTCAATCACTGAGCTCTCTCTCTTTGGAATGGAATCC 3037
2824 CTTCTCTTTGAAGATTTCAATCACTGAGCTCTCTCTCTCTTTGGAATGGAATCC 2883
3038 CGAGCCAGCCAGATGAGATTTTGAAGATGATGATGATGATGATGATGATGATGATG 3097
2884 CTACCATCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2943
3098 CATGATTAATGAGCCCTCTGTAGATTTGAAGATTTCTGCAACAGACAGGATGAT 3157
2944 CATGATTAATGAGCCCTCTGTAGATTTGAAGATTTCTGCAACAGACAGGATGAT 3003
3158 TAAAAATTTAATTTCAAGCTGATGATGATGATGATGATGATGATGATGATGATG 3217
3004 TAAAAATTTAATTTCAAGCTGATGATGATGATGATGATGATGATGATGATGATG 3063
3218 GATCAAGAGTCAATTTCAAGAGAGAGTCAAGCTGATGATGATGATGATGATGATG 3277
3064 GATCAAGAGTCAATTTCAAGAGAGAGTCAAGCTGATGATGATGATGATGATGATG 3108
3278 CACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3337
3109 -----AAGTGAACCACTTTATTCAGAAAGATGATGATGATGATGATGATG 3147
3338 CTGAGCTGCTGAGCTTATGCTCAATTTATGATGATGATGATGATGATGATGATG 3397
3148 CAGCTGCTGCTGAGCTTATGCTCAATTTATGATGATGATGATGATGATGATGATG 3207
3398 ACTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3457
3208 ACTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3267
3458 ATGTGCTCTGAGCTTCTTTGATTTAAAGGCTTAATCCAGAAACAGATTAAGTTC 3517
3268 ATGTGCTCTGAGCTTCTTTGATTTAAAGGCTTAATCCAGAAACAGATTAAGTTC 3327
3518 GAGTGTGCTGT 3577
3328 GAGTGTGCTGT 3387
3578 CAGGATGAGCAAGCCGAGAGGATTTGCAACTCAGGAGCTGATGATGATGATGATG 3637
3388 CAGGATGAGCAAGCCGAGAGGATTTGCAACTCAGGAGCTGATGATGATGATGATG 3447
3638 GTGCTGTGCTCTCTTATTTATTTATTTGATGATGATGATGATGATGATGATGATG 3697
3448 GTGCTGTGCTCTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTAT 3507
3698 GTGATTAATTTCACTTAAAGAAAGATGATGATGATGATGATGATGATGATGATG 3757
3508 GTGCAAAATTCATGATGAAGAAAGATGATGATGATGATGATGATGATGATGATG 3567

QY 3758 TGAAGAGATGATGAGACATTTGAGAAATACAGTATGACAGAGACCAAGCCCTTTGA 3817
DB 3568 TGAAGAGATGATGAGACATTTGAGAAATACAGTATGAGAGAGACCAATTAACCTCTA 3627
QY 3818 AAAAGAGAGTGCACATCTCTTCAGACAGACGTGTGAAAAAGAGTATGTAGACAGACCC 3877
DB 3628 AAAAGAGAGTGCAGACCCGTACAGACAGACGTGTGAAAAAGAGTATGTAGATGATTT 3687
QY 3878 TAGTTACTATGAGAGAGGGGTAAATGCGCAGTTCAATGAGATGAGTGGCTCTTATTTGAGC 3937
DB 3688 TAGTTACTATGAGAGAGGGGTAAATGCGCAGTTCAATGAGATGAGTGGCTCTTATTTGAGC 3747
QY 3938 AATACAGTGTAAAGAAAGAGAAAGACCGCTGAGAGAAACGAAGCTGAGAGCACCTT 3997
DB 3748 AATACAGCGGTAAAGAAAGAGAAAGACCTGACAGAGAAATGAAAGTTCTGAGGCTCTT 3807
QY 3998 CTCCTGTCAAGCAGATGATTTCTTTTATTTTAACTCAAGCCCAAT 4051
DB 3808 CTCCTGTAAATGCCATGAATTCATTTGTGTAAATCAAGAACTTGATTCCTTGT 3861

RESULT 8

AAZ38181
ID AAZ38181 standard; DNA; 1371 BP.

XX AC AAZ38181;

XX DT 14-FEB-2000 (first entry)

XX DE Human Nr-CAM gene fragment.

XX Nr-CAM; neuron-glia-related cell adhesion molecule; cell proliferation;
XX tumorigenesis; malignancy; cancer; leukemia; hyperproliferative disorder;
XX degenerative disorder; growth deficiency; trauma; wound; tumor; diabetes;
XX systemic lupus erythematosus; demyelinating disease; growth; human; ss.

XX OS Homo sapiens.

XX PN MO995380-A1.

XX PD 04-NOV-1999.

XX PF 27-APR-1999; 99MO-US009039.

XX PR 27-APR-1998; 98US-0083152P.

XX PR 14-DEC-1998; 98US-0112098P.

XX (PACT-) PACIFIC NORTHWEST CANCER FOUND.

XX PI Murphy GP, Boynton AL, Sehgal A;

XX DR WPI; 2000-023268/02.

XX Use of neuron-glia-related cell adhesion molecule for developing agents
XX for the diagnosis and treatment of e.g. cancers, hyperproliferative
XX disorders, growth deficiencies, degenerative disorders, trauma or wounds.
XX Example; Page 181-182; 183pp; English.

XX The invention relates to the use of neuron-glia-related cell adhesion
XX molecule (Nr-CAM) as a marker for diagnosing, treating, inhibiting or
XX preventing disorders involving cell proliferation. An antisense nucleic
XX acid complementary to at least a portion of an RNA transcript of a Nr-CAM
XX gene can be used to inhibit hyperproliferation of a tumor cell, for the
XX treatment of tumorigenesis. Agents which inhibit and promote Nr-CAM
XX function can be used for the treatment of various diseases and disorders
XX (see AAZ38152 for a detailed description). The products can also be used
XX for detection, diagnosis and production of animal models. The present
XX sequence represents a human Nr-CAM gene fragment

XX Sequence 1371 BP; 438 A; 313 C; 281 G; 339 T; 0 U; 0 Other;

XX Query Match 33.2%; Score 1371; DB 3; Length 1371;

Best Local Similarity 100.0%; Pred. No. 0;
Matches 1371; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 130 ATGCCGAAAAGAAAGCGCTTAATCTGCGGGAGAGAGCCCTGATTTCTTCCGTGCGCAG 189
DB 1 ATGCCGAAAAGAAAGCGCTTAATCTGCGGGAGAGAGCCCTGATTTCTTCCGTGCGCAG 60
QY 190 ATGATTAGTGCACTGGAAGTACTCTTGTATCCAAACTCTTGAAGACTTGGTACAGCT 249
DB 61 ATGATTAGTGCACTGGAAGTACTCTTGTATCCAAACTCTTGAAGACTTGGTACAGCT 120
QY 250 CCAACCATCACCACACAGTCTTCCAAAAGTTTACATTATTTAGACCTTCGGGAGAAATTTGTA 309
DB 121 CCACCATCACCACACAGTCTTCCAAAAGTTTACATTATTTAGACCTTCGGGAGAAATTTGTA 180
QY 310 ATCCAGTGTGAAGCCAAAGGGGAAACGGCCCCAGCTTTTCTGTGACCCGTAAATGGAGCT 369
DB 181 ATCCAGTGTGAAGCCAAAGGGGAAACGGCCCCAGCTTTTCTGTGACCCGTAAATGGAGCT 240
QY 370 CATTTTGAACATGATTAAGACCCCTGTGTCAACATGAAGCCTGGCAGAGAAACGCTCATTA 429
DB 241 CATTTTGAACATGATTAAGACCCCTGTGTCAACATGAAGCCTGGCAGAGAAACGCTCATTA 300
QY 430 ATTAACATCAGTGAAGGAGAGGAAAGCTGAGACCTTATGAAGAGTCTATTCAGTTCACGA 489
DB 301 ATTAACATCAGTGAAGGAGAGGAAAGCTGAGACCTTATGAAGAGTCTATTCAGTTCACGA 360
QY 490 AGGAAGCAAGCGGGAGCTGCAAGTTTCTAATACATGTTGTGTCGGCCATCCAGATCACCA 549
DB 361 AGGAAGCAAGCGGGAGCTGCAAGTTTCTAATACATGTTGTGTCGGCCATCCAGATCACCA 420
QY 550 TTGTGACCAAGAAAGAAACCTTGAAACCAATCACTTCAAGTGTCACTTCTTACTACT 609
DB 421 TTGTGACCAAGAAAGAAACCTTGAAACCAATCACTTCAAGTGTCACTTCTTACTACT 480
QY 610 CCTCGAAGCCCCCAATTGATTAACACCACTAATATTTTGGATGAGATTAATTCCTTT 669
DB 481 CCTCGAAGCCCCCAATTGATTAACACCACTAATATTTTGGATGAGATTAATTCCTTT 540
QY 670 CAAAGACTTCCCAAGGAGAGAGTCTTCTAAGTTTGAATGGGACCTTATTTTCC 729
DB 541 CAAAGACTTCCCAAGGAGAGAGTCTTCTAAGTTTGAATGGGACCTTATTTTCC 600
QY 730 AATGTCCTCCAGAGAGACACCGCGAAGACTATATCTGTATGTAGATTAATCACTACT 789
DB 601 AATGTCCTCCAGAGAGACACCGCGAAGACTATATCTGTATGTAGATTAATCACTACT 660
QY 790 CAAACCATACAGAGAGACCTTATTTCTGTGAAGGTGATTTCTGTGATGAATTTGAAT 849
DB 661 CAAACCATACAGAGAGACCTTATTTCTGTGAAGGTGATTTCTGTGATGAATTTGAAT 720
QY 850 GACACTATAGCTGCTAATTTTGTAGTACCTGAGTTTATGGTCTAATCAAGTAGAGAG 909
DB 721 GACACTATAGCTGCTAATTTTGTAGTACCTGAGTTTATGGTCTAATCAAGTAGAGAG 780
QY 910 AGGCCACCAAACTTTTAACTCCAGAGGCAATGACAAATCAAGAGAAATTAAGAGA 969
DB 781 AGGCCACCAAACTTTTAACTCCAGAGGCAATGACAAATCAAGAGAAATTAAGAGA 840
QY 970 AATGTCCTTCACTGAGAGTCAATTCAGAGAGACTGCTTACCCCAATTTTACTGCGCA 1029
DB 841 AATGTCCTTCACTGAGAGTCAATTCAGAGAGACTGCTTACCCCAATTTTACTGCGCA 900
QY 1030 AAGGAAGTGAAGTCTCCCAAAAGAGAGAGTCTTGAAGAACTTTGAGAGAAACCTTG 1089
DB 901 AAGGAAGTGAAGTCTCCCAAAAGAGAGAGTCTTGAAGAACTTTGAGAGAAACCTTG 960
QY 1090 CAGATCATTCATGTTTCAAGAGCAGACTCTGGAATTAACATGTATAGCAAAAAATGCA 1149
DB 961 CAGATCATTCATGTTTCAAGAGCAGACTCTGGAATTAACATGTATAGCAAAAAATGCA 1020
QY 1150 TTAGAGCCATCCACCATACATTTCTGTAGATTAAGCGGCTCCATCTGATCACA 1209

Db 1021 TTAGAGCCATCCACCATTCATTTCTGTTAGATTAAAGCGCTCCATCTGATCACA 1080
 QY 1210 GCCCCTCAAAATCTTGCTGTGCTCCAGAGAGATGGAGCTTGATCTGACAGCTAAT 1269
 Db 1081 GCCCCTCAAAATCTTGCTGTGCTCCAGAGAGATGGAGCTTGATCTGACAGCTAAT 1140
 QY 1270 GGCAACCCCAAAACCCAGAAATAGCTGTGTTACAAATGAGTCCCAATATAAAATGGCCCT 1329
 Db 1141 GGCAACCCCAAAACCCAGAAATAGCTGTGTTACAAATGAGTCCCAATATAAAATGGCCCT 1200
 QY 1330 GATGACCCCAAGCAAAATTAATAGCCGATACCATTTATTTTCAATGTTCAAGAAAGA 1389
 Db 1201 GATGACCCCAAGCAAAATTAATAGCCGATACCATTTATTTTCAATGTTCAAGAAAGA 1260
 QY 1390 TCAGTGCAGTATATCAAGTCAATGCTCTTAATGATATGATATTACTGGCAACGCA 1449
 Db 1261 TCAGTGCAGTATATCAAGTCAATGCTCTTAATGATATGATATTACTGGCAACGCA 1320
 QY 1450 TTTGTAATGTCGTGGCTGAGCCACACCAATCTCTACACCTGCAAAACACA 1500
 Db 1321 TTTGTAATGTCGTGGCTGAGCCACACCAATCTCTACACCTGCAAAACACA 1371

RESULT 9

AAZ38182 standard; DNA; 1371 BP.

AAZ38182;

14-FEB-2000 (first entry)

Rat Nr-CAM gene fragment.

Nr-CAM, neuron-glia-related cell adhesion molecule; cell proliferation;
 tumorigenesis; malignancy; cancer; leukemia; hyperproliferative disorder;
 degenerative disorder; growth deficiency; trauma; wound; tumor; diabetes;
 systemic lupus erythematosus; demyelinating disease; growth; rat; ss.

Rattus norvegicus.

W09955380-A1.

04-NOV-1999.

27-APR-1999; 99WO-US009039.

27-APR-1998; 98US-0083152P.

14-DEC-1998; 98US-0112098P.

(PACI-) PACIFIC NORTHWEST CANCER FOUND.

Murphy GP, Boynton AL, Sehgal A;

WPI, 2000-023268/02.

Use of neuron-glia-related cell adhesion molecule for developing agents
for the diagnosis and treatment of e.g. cancers, hyperproliferative
disorders, growth deficiencies, degenerative disorders, trauma or wounds.

Example; Page 182-183; 183p; English.

The invention relates to the use of neuron-glia-related cell adhesion
molecule (Nr-CAM) as a marker for diagnosing, treating, inhibiting or
preventing disorders involving cell proliferation. An antisense nucleic
acid complementary to at least a portion of an RNA transcript of a Nr-CAM
gene can be used to inhibit hyperproliferation of a tumor cell, for the
treatment of tumorigenesis. Agents which inhibit and promote Nr-CAM
function can be used for the treatment of various diseases and disorders
(see AAZ38152 for a detailed description). The products can also be used
for detection, diagnosis and production of animal models. The present
sequence represents a rat Nr-CAM gene fragment

Sequence 1371 BP; 403 A; 339 C; 291 G; 338 T; 0 U; 0 Other;

Query Match 26.4%; Score 1092.6; DB 3; Length 1371;
 Best Local Similarity 87.3%; Pred. No. 1.9e-311;
 Matches 1197; Conservative 0; Mismatches 174; Indels 0; Gaps 0.

QY 130 ATGCCGAAAGAAAGCGCTTAATCTGCGGAGAGTGGCCCTGATTTCTTCTGTCGAG 189
 Db 1 ATGCCGAAAGAAAGCGCTTGTCTGACAGAGGCGCCCTGTCTTCTCTGTCGAG 60
 QY 190 ATGATTAATGCACTGGAAGTACCTCTTGAATCAAAACCTTCTGGAAGTCTGTAACAGCT 249
 Db 61 ATGATCAAGCGCTGGAATGTTCTCTTGAATCAAAAGCTCTTGAATGACCTGTAACAGCT 120
 QY 250 CCAACCATCAACCAACAGCTCTCAAAAGATTACATTTATGACCCCTGGGAGAAATTTGTA 309
 Db 121 CCAACTATCACTCAACATCAACCAAAAGATCAATGATTAAGCCAGCGGAGAAATTTGTA 180
 QY 310 ATCCAGTGTGAAGCCAAAGGAAACCGCCCAAGCTTTTCTGTGACCCGTAATGGGACT 369
 Db 181 ATCCAAATGTGAGGCCAAAGGAAACCTCTCAAGCTTTTCTGTGACTGTAAACGGAACA 240
 QY 370 CATTTTGACATCGATTAAGAACCTCTGTGTCAACATGAAGCCTGGACAGAAACGTCATA 429
 Db 241 CATTTTGACATGAACAAAGACCTCTGTGTCAATGAAGCCTGGTCAGAAACCTTGTGC 300
 QY 430 ATTACATCATGAGCGAAGGAAAGGAAAGCTGAGACTATGAAGAGTCTATCACTGATCAGCA 489
 Db 301 ATCAACATCATGATGAGGAAAGGAAAGGCGAGACCTATGAAGGAGTTTACCACTGACCTGCA 360
 QY 490 AGGAACGAAGCGGAGCTGCAAGTTCCTAATAACATTTGTCGCGCCATCCAGATCACCA 549
 Db 361 AGGAATGAGCGCGGAGCTGTGTCTCAATAACATTTGTCGCGCCCTTAAGGTCAACC 420
 QY 550 TTGAGACCAAGAAAGAACTTGAACCAATCACTTCAAGTGGTCACTTTAGTACTT 609
 Db 421 TTGAGACCAAGAAAGAACTTGAACCAATCACTTCCAGAGTGGTCACTTACTACTA 480
 QY 610 CCTGACAGACCCCAATTTGATTAACACACCTTAATATTTTGGATGATTAATCCCTT 669
 Db 481 CCAATGAGGCTTCAATTTGATTAACACCGGCTAATATTTTGGATGATTAATCCCTT 540
 QY 670 CAAGACTTCCCAAAAGTGAAGAGATTCTCAAGTGTGAATGGGACCTTTATTTTTC 729
 Db 541 CAAGACTTCCCAAAAGTGAAGAGATTCTCCAAAGACTGAATGAAGACCTTTACTCTCC 600
 QY 730 AATGTCCTCCAGAGGACACCCGGAGACTATATCTGTATGCTAATTTATCATCT 789
 Db 601 AATGTCCTCCAGAGGACACCCGGAGACTATATCTGTATGCTAATTTATCATCACT 660
 QY 790 CAACCAATACAGCAAGCAACCTATTCTGTGAAGGATTTGATGATGATGAATTAAT 849
 Db 661 CAACCAATTAACAGAAACCAACCTATTCTGTGAAGGATTTGATGATGATGAATTAAT 720
 QY 850 GACACTATAGCTGCTAATTTGATGACACTGATGTTTATGCTGAATCAAGTAGAGAG 909
 Db 721 GACACTATAGCTGCTAATTTGATGACACTGATGTTTATGCTGAATCAAGTAGAGAG 780
 QY 910 AGGCCACCAACATTTTAACTTCCAGAGGCAATGCAAGTAACAAGAGAAATTAAGAGA 969
 Db 781 AGGCCACCAACATTTTAACTTCCAGAGGCAATGCAAGTAACAAGAGAAATTAAGAGA 840
 QY 970 AATGCTTTTACAGTGAATGATTTGCAAGAGACCTGCTACCCCAATTTATTTCTGGGCA 1029
 Db 841 AATGCTTTTACAGTGAATGATTTGCAAGAGACCTGCTACCCCAATTTATTTCTGGGCA 900
 QY 1030 AAGGAAGATGAAATGCTAACCMAAAGAGACAGTCTTAAGAACTTTGAGAAACCTTG 1089
 Db 901 AAGGAAGATGAAATGCTTCCGTGACCGGAGCTTTTATGGAACCTTTAAGAAACCTTG 960
 QY 1090 CAGATCATTAATGTTTCAAGAGCACTTGGAAATTAACCAATGATTAAGCAAAATGCA 1149
 Db 961 CAGATCATTAATGTTTCAAGAGCACTTGGAAATTAATCAATGATTAAGCAAAATGCA 1020

QY 1150 TTAGAGCCATCCACCATCATTTCTGTAGTTAAAGCGCTCCATCTGATCACA 1209
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 DB 1021 TTGGAGCGCGTCCATCATTCATTTCTGTACAGTTAAAGCGCTCCATCTGATGTT 1080
 |||
 QY 1210 GCCCTCAAAATTTGTGCTGTCCCAAGAGAGATGGAGCTTGAATCTGCAGAGCTAAT 1269
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 DB 1081 GCACCTTCACAACTCTGTCTTCCCAAGAGAGATGGAGCTTGAATCTGCAGAGCTAAT 1140
 |||
 QY 1270 GGCACCCCAAAACCCAGAAATTTAGCTGTTAAACAAATGGATGCCATAGAAATGGCCCT 1329
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 DB 1141 GGCACCCCAAAACCCAGAAATTTAGCTGTTAAACAAATGGATGCCATAGAAATGGCTTC 1200
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 QY 1330 GATGACCCAGAGAAAATAGATGCGATACCATTAATTTTCAATGTTCAAGAAAGA 1389
 |||
 DB 1201 GATGACCCAGAGAAAATAGATGCGATACCATTAATTTTCAATGTTCAAGAAAGC 1260
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 QY 1390 TCAAGTGCAGTATATCATGTCGAATGCTCTTAATGAATATGATATTTACTGGCAACGCA 1449
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 DB 1261 TCAAGTGCAGTATATCATGTCGAATGCTCTTAATGAATATGATATTTACTGGCAATGCA 1320
 |||
 QY 1450 TTTGTAAATGTGCTGAGCGAGCAGCAGCAATCTCTCAACCTGCAACCAACA 1500
 |||
 DB 1321 TTTGTAAATGTGCTGAGCGAGCAGCAGCAATCTCTCAACCTGCAACCAACA 1371
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RESULT 10
 AAD49596
 ID AAD49596 standard; cDNA; 4360 BP.
 AC AAD49596;
 XX
 DT 24-MAR-2003 (first entry)
 XX
 DE Human cytoskeleton-associated protein, CSAP-7 cDNA.
 XX
 KW Human; cytoskeleton-associated protein; CSAP-7; atherosclerosis; cancer;
 KW gene therapy; gene; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key
 FT Location/Qualifiers
 FT 276..4355
 FT /*tag= a
 FT /product= "Human CSAP-7"
 FT sig_peptide
 FT 276..353
 FT /*tag= d
 FT sig_peptide
 FT 276..347
 FT /*tag= b
 FT mat_peptide
 FT 348..4352
 FT /*tag= c
 FT /product= "Human mature CSAP-7 protein"
 FT mat_peptide
 FT 354..4352
 FT /*tag= e
 FT /product= "Human mature CSAP-7 protein"
 FT
 FT
 PN WO200279404-A2.
 XX
 PD 10-OCT-2002.
 XX
 PF 25-MAR-2002; 2002WO-US009288.
 XX
 PR 29-MAR-2001; 2001US-0280508P.
 PR 03-APR-2001; 2001US-028123P.
 PR 13-APR-2001; 2001US-0283769P.
 PR 04-MAY-2001; 2001US-028609P.
 PR 10-MAY-2001; 2001US-0290518P.
 PR 18-MAY-2001; 2001US-0291870P.
 PR 29-MAY-2001; 2001US-0294451P.
 XX
 PA (INCY-) INCYTE GENOMICS INC.
 XX
 PI Hafalia Aja, Tang TY, Yue H, Khan FA, Ison CH, Baughn MR,
 PI Warren BA, Dugan BM, Thangavelu K, Honchell CD, Azimzai Y;

PI Elliott VS, Burford N, Ding L, Yue H, Becha S, Emerling BM;
 PI Richardson TW, Lee SY, Bandman O, Lai PG, Lee S, Gietzen KJ;
 PI Malia NK, Griffin JN, Lee EA, Swarnaker A, Ring HZ, Jones KA;
 XX
 DR MPI: 2003-092894/08.
 DR P-PSDB: AAE32109.
 PT New human cytoskeleton-associated proteins, useful for preparing a
 PT composition for diagnosing or treating a disease or condition associated
 PT with decreased expression or overexpression of functional CSAP e.g.,
 PT cancer.
 XX
 PS Claim 5: Page 210-211; 233pp; English.
 CC The invention relates to new human cytoskeleton-associated protein (CSAP)
 CC and its polynucleotide. The polypeptide is useful for preparing a
 CC composition for diagnosing or treating a disease or condition associated
 CC with decreased expression or overexpression of functional CSAP e.g.,
 CC atherosclerosis or cancer. The present sequence is human CSAP-7 cDNA. The
 CC invention is useful in gene therapy
 XX
 SQ Sequence 4360 BP; 1067 A; 1321 C; 1185 G; 787 T; 0 U; 0 Other;

Query Match 18.9%; Score 779.8; DB 7; Length 4360;
 Best Local Similarity 54.6%; Pred. No. 1.1e-218;
 Matches 1701; Conservative 0; Mismatches 1387; Indels 29; Gaps 6;

QY 167 CCCTGATTCCTCTCCCTGCGCAGATGATTAGTGCAGTGAAGTACTCTGTGTCGAAC 226
 |||
 DB 313 CTTCTCCTCTGCTCCTCCTCCTGCTGTTGGCGAGCATGAAATTCATGATTCAGCA 372
 |||
 QY 227 TTTCTGAAGACTTGTGTAGAGCTCTCAACCATCACCAAGTCTTCAAGATTACATTA 286
 |||
 DB 373 TTCAGAAAGAGCTGAGCGAGCGGCCAACCATCACCAAGTCTTCAAGATTACATTCG 432
 |||
 QY 287 TTGACCTCTGGGAGAAATTTGTAATCCAGTGTGAAGCCAAAGGAAACCGCCCAAGCT 346
 |||
 DB 433 TGGACCCCGTGATTAACATCTGATTTGAGTGAAGCAAAAGGAAACCTGCCCCAGCT 492
 |||
 QY 347 TTTCTGAGACCGGTATGGGACTCATTTTGAATGATTAAGAACCTGTGTCACATGA 406
 |||
 DB 493 TCCACTGACACGAAACAGACGATTTCTTCAATGTCGCAAGAACCCCGGGTGTCAATGA 552
 |||
 QY 407 AGCCTGACACGAAAGCTCATTAATTAATCATGATGAGGAGGAAAGTGAAGCTATG 466
 |||
 DB 553 GAGAGAGCTGTGAGACCTGTGTGATTCCTCGAGTGGGGGGGGGCGAGGAAATNG 612
 |||
 QY 467 AAGAGTCTATCATGTGTACAGCAAGAAAGAAAGCGGAGCTGCACTTCTTAATAATTG 526
 |||
 DB 613 AAGGAGAAATATCATGCTTCCGCGCAACAAATTTGGCAAGCGCCCTGTCTCAATAGATCC 672
 |||
 QY 527 TTGTCGGCCCATCCAGATCAACCATGTTGGAGCCAAAGAAACTTGAACCAATCACACTTC 586
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 DB 673 GCTTCAGGTGTCTAAATCTCTCTGTGGCCCAAGAAACCTTAAGCCTGTCTGTGCTCC 732
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 QY 587 AAGAGTGTCACTTTAGTACTTCCCTGAGAGCCCAATTTGATTAACCACTTAATA 646
 |||
 DB 733 AAGAGGGGCTCTTTGAAGCTCAAGTGAACCCCGCGCTGGAATTCATCCCGGTCA 792
 |||
 QY 647 TATTTTGAATGATTAATCTCTTCAAGACTTCAAGAAAGTGAAGAGTTTCTCAAGTT 706
 |||
 DB 793 TCTTCTGATGAGCAGCTTCATGAGAGCCATCAACCAAGCAAGAGTGTCTCTGAGGCC 852
 |||
 QY 707 TGAATGGGAGCTTATTTTTCATATGCTCCAGAGAGACCCGCGAGACTATATCT 766
 |||
 DB 853 ATTAAGGAGACTTAATCTTCAAGAGTGTGAGAGACGAGACCGACTACATTT 912
 |||
 QY 767 GTTATGCTAGATTATATCACTCAAAACATACAGAGAAAGCACTTATTTCTGTGAAG 826
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 DB 913 GTTAAGCCCGCTTCACTTCAACCAACATCCAGACAGAAAGAACCTTTCAACCTCAAG 972
 |||
 QY 827 TGATTCAGTGATGAATGAATGAACACTATAGCTGCTAATTTGATGAAGTCACTGAGTTT 886
 |||

Db 973 TCCTCAACCAACCCCTTAATTAATGAC-----TCGTCCTTAAGAAACCAACCTGCATGT 1026
Qy 887 ATGTGCTAATATCAATAGAGAGGCAACCAATTTTAACTCCAGAGCAATGCA 946
Db 1027 ACGTGTCCCGAGAGAGTTGCGAAGAAACCAAGCTTCATGATCCCGAGGCAACCGCA 1086
Qy 947 GTAACAAAGAGAAATTAGAGAAATGTGCTTCACTGAGTGATGAGAGAGAGCTGC 1006
Db 1087 GGAGCCAGATGGTGCTTCGTGGCATGACCTCTGCTGGAAATGCAATGCTCCGGGTGC 1146
Qy 1007 CTACCCCAATTATTAATCTGGGCAAGAGAAATGCAATGCTACCCAAAACAGACATTT 1066
Db 1147 CAACACCAACATCGCATGTATCAAGAAAGTGCGGCACTCCCATCTGTATAGGCCAAT 1206
Qy 1067 ATPAGAACTTTGAGAAACCTTGAGATCAATTCATTTTCAAGAGAGACTCGAAT 1126
Db 1207 TTGAGAACTTTAATAGGCTGCTGCTGATCAAAATCTCTGAGAGAGACTCCGGGAGT 1266
Qy 1127 ACCAATGTATAGCAAAAATGCAATTAAGAGCCATCCACATACATTTCTGTAGATTA 1186
Db 1267 ATTTGCTGCTGGCTCCCAACAGATGGGAGAGATCCGGGAGATCTGGTGAGATTA 1326
Qy 1187 AAGCGCTCATATCTGATGACAGCCCTCAAAATCTTGTGCTGCTCCAGAGAGATG 1246
Db 1327 AAGCTGCTCTTAATGCTGAGAGCAACCAAGAACTTATCTGCTCTGGGAGAGATG 1386
Qy 1247 GGACCTGTATGAGAGGTAATGAGCAACCCAAACCCAGAAATTAAGCTGTATTAACAATG 1306
Db 1387 GGAAGCTGTGTGTCAGGCAATGAGAAACCCCAACCTGCTCCAGTGAATGATG 1446
Qy 1307 GAGTCCCAATAGAAATTTGCCCTGATGACCCCGAGAGAAATAGATGCGATACCATTA 1366
Db 1447 GGGAACTTTGCAATGGGCAACCACTTAACCAACCGTGAAGGCGGAGACACATCA 1506
Qy 1367 TTTTTCATATGTTCAAGAAAGATCAAGTGCAGTATATGATGCAATGCTCTAATGAT 1426
Db 1507 TCTTCGGGACACCCGATCAGAGAGGCTGTGTATCCAGTGCAACCTCCACAGAGC 1566
Qy 1427 ATGGAATTTATGCGAAGAGCAATTTGTAAATGTGTGCTGAGCCACAGCAATCTCA 1486
Db 1567 ATGGCTACCTGCGCAAGCGCTTTGTGATGTGTGATGTGCGCTCGAGATGCTGT 1626
Qy 1487 CACTGCAACACACTCTACAGGTCAATGCAAAACAGGCTGCTTACTAGATGCTGT 1546
Db 1627 CGCCCCGAGAACAGCTCATTTCAAGATTTCTTACACAGGAGCGGGCTGAGTCCCTT 1686
Qy 1547 TCTTTGGGTCTCTCTCCCAACATCGAGTGTAAAGAGCTAAAGAGTGTCTTTC 1606
Db 1687 TCTTTGGGTCTCCATCCCACTGCGATGTTTAAAGATGGGCAAGAGCAACCTGG 1746
Qy 1607 ATGGAATATTTATGTTTACATGAAATGGAACCTTGGAAATCAAGATGCTACATGGA 1666
Db 1747 ATGGTGGCACTACCAATGTTTATGAGAAAGGCAAGTCTGGAAT-7AAGATGATCCGCAA 1805
Qy 1667 TCGTTAAAGAAATTCCTGTGGCCAAAGAGACAGTACAGAACTTTAAGTGTGCA 1726
Db 1806 GAGGACAGGGGATCTACACTGTGTGCGCACCAACATCTGGGCAAACTGAAACCA 1865
Qy 1727 GGAATTAATTAAGGATGCGAAAGATGAAATTC-ACCTACAGCCGCAATATGCAATTTG 1785
Db 1866 GTCCGCTGAGGTCAAAAGACCCCAAGATCTACCGATGCGGAGAGCAAGGTGCTC 1925
Qy 1786 CAAAGAGGAGATGTGTCTTTGAATGCAAGTGAACATGATCAACCTTATCCCTC 1845
Db 1926 AGAAGGGGACACAGGTGAGCTGTGAGTGTGGGTGAACAGACCCCTCTGAAACCTC 1985
Qy 1846 ACTGTCTGTGCTGAAGACAAACAGGAATGCGCCAGATGAAAGATTCCTGTGAC 1905
Db 1986 ACCGTCTCGGTGAAGATGACAGCCGCTCTATATTGGAACAGAGATGAAGAGAA 2045
Qy 1906 AAGATCATCTATGTGTAGCTGATGTCAATGACATGACAGCGGAGCTTACAGTGTGTG 1965
Db 2046 GACGACTCCCTGACCATCTTTGGGGGTGGCAGAGCGGAGCAAGGGAGTTACAGTGTGTG 2105
Qy 1966 GCCAACACCACTGTGAGAGAGCTCTCCGCAAGCGGTGTGCTTAAAGCTTGTCTACT 2025
Db 2106 GCCAGACCCAGAGCTAGACCAAGACCTGGGCAAGGCTTAACCTGATGATGAG 2165
Qy 2026 CCAACTCCAGCTCCCGTTTACATGTCT-----CCAAATCTCTCTTTGAC 2070
Db 2166 GCCACTCCAACTAACCTGTTGGCTGCTCCGCAAGAGAGCGGACAGCGGCCGGGAG 2225
Qy 2071 TTGAACTGACAGATCAACTTGAACAAAGTGTGAGCTGTATGAGACCCAGGAGATGAC 2130
Db 2226 CTGAGCTGACCGAGCTGGCCAGAGAGCGGTGCGTGAACCTGATCTCCGGGATGCT 2285
Qy 2131 AACATAGCCCACTTACAAATTTCAATTCATGCAATTAATGAAGATGCAATGACAAAGCGAG 2190
Db 2286 AACAAAGCCCACTACAGATCAAGCTGTGCTGCTGCAATTTGAAGAGACAGTTCACACTGG 2345
Qy 2191 CTGTGGCAACCAAACTGAAGTTTCTGGAACAGACCAAGCCAGCTGAAGCTGTCT 2250
Db 2346 GTCTGGCATGACATTTCAAGTACCAGGAGCGTTAACTGAGCGCTCTCCGGCTGTCC 2405
Qy 2251 CTTTACGTGAATCTCTCTCCGCTGATGTGAGTGAACAGATTTGGGAGAGCTTGGCC 2310
Db 2406 CCGTATGTCACTACAGATTCGCTGTCAATTCATCAACAGAGTTGGAGAGAGCAACCC 2465
Qy 2311 AGCGAGCGGTGACAGATTTGACGAAAGCCTGAGAACAGATTAACCCCAAGCT 2370
Db 2466 AGCTCCCATCCGAGCGCTACAGAACAGTGAAGACCCCGAGTCCATCTGTGTAC 2525
Qy 2371 GTGGAAGACCTGGATCAGAGCTGATTAATTTGAGATTAAGTGAAGCCTTGAATGCT 2430
Db 2526 GTGAAGGAGAGGGAGACAGAAAGAACATGAGATCAAGTGAACCCCATGATGCC 2585
Qy 2431 TTGGAATTAATGGGCGAGCTTTAGTACAAAGTTACTGGCGGCAAAAGATGAT 2490
Db 2586 ACTCGGCTTTGGGCCCAACCTGCGTACATTTGCAAGTGAAGCGGAGAGACTGGA 2645
Qy 2491 GATGAATGACATCTGTGGTTGTGCAATGATCAAAATTAATGTCTCAAGGACGCA 2550
Db 2646 GAGGCTGGAACAGTCAAGTGTG---GGGCTCTGCTAGTGTGGGAGAGACCCA 2702
Qy 2551 ACCTTTGTTCATACCTGATCAAAAGTTGAGGCGCTGAATGACATGAGGTTTGGCCCGAG 2610
Db 2703 GTCTAGTGCCCTTAAGATCCAGATCCAGGTGAATTAATGACTTGGGAGGCGCTGAG 2762
Qy 2611 CGAGCTGATGATGGAACATTTGAGAGAGACTCTCCAAATGTGTGCTGAGGAGCTG 2670
Db 2763 CCAAGTCCGTATGTTTACTCCGAGAGAGTTATCCAGGGCTGCGCCCACTGAAGTT 2822
Qy 2671 CGTGTGAATGTGTGATCAGTACCTTACCGAGGTGCACTGGGACCCAGTACCTCTGAA 2730
Db 2823 AAAGTCCGATATTAACAGAGACAGCAACCACTTCAAGTGAACCGGTCTACTCCGAC 2882
Qy 2731 AGCATCCAGAGACCTTCAAGGCTATGCAATTTACTTATGGAAGACCCAGAGTTCACT 2790
Db 2883 ACGTTCAGGGCAGCTCAGAGATGACAGAGCTTACTTGAAGGAGAGAGAGCTTGGCTG 2942
Qy 2791 AAAAGAAACAGAGTCACTGAAGAAATCTCTCAACCTTTCAAAGGAGAGACTAT 2850
Db 2943 AAGAACTGTGGTGTCTCAGAAAGAGACAGAAAGCACTTCCCTGTGAGACCGCTCGT 3002
Qy 2851 GGCATGTTGCGGGGCTTGAAGCCCTTTAGCCACTACACATGAATGTCGAGTGTCAAT 2910
Db 3003 GCGGTGTGTCCGCTCTTCCCTCAAGTATCTACAAAGCTGAGATGTGTGTGATCAAT 3062
Qy 2911 GGGAAAGGGAGGGGCCAGCGCTGACAGAGCTTAAATCTCCAGAAAGAGTCCCG 2970
Db 3063 GGGAGAGGTGATGGGCTCGAGTGAAGACAAAGAGTTCAACACCCGGAGAGAGTACCC 3122
Qy 2971 AGTGTCTCTGTCTTTGAAGTTGTGAATCAACATGAGACTCTCTCACTTTGGAATG 3030
Db 3123 AGTGCCTCTTAAGCGTTTCCAGTGTGCGGAGCCCAACTGAGAGACAACTGAATG 3182

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Oy 3031 GATCCACCGAGCCAGCCGATTTTGAAGAGTACAGCTTAAGTACAGCCATT 3090
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Oy 3091 AACAGCACATGATTAATGAGCCCTCTGTGATGATTTGAAAAATTCCTGCCAACAAGACGCG 3150
Db 3243 AACGGGAC---CAAACTAGAGAAAGAGATGAGAAACTCTCTCCATCAGACCAAG 3299
Oy 3151 TGGACCTTTAAAAATTTAAATTTACACACTCCGATATTAAGTTTATTTCTATGCAACAACA 3210
Db 3300 TTCACGGTCCAAAGAAAGAGACCCCGTGTACCGCTTACCGCTTTACCTTCAGCCGACAGGACG 3359
Oy 3211 TCAGCAGATCAAGAAAGTCAAAATTAACAGAGAGAGTAAACAATCTGTGATGAAGCT 3267
Db 3360 CAGGTGGGCTCTGGGGAAGCCGTCACAGAGAGTACACAGACCCCGAATGAAGCT 3416

RESULT 11
AAD49595
ID AAD49595 standard; cDNA; 4080 BP.
AC AAD49595;
XX
XX 24-MAR-2003 (first entry)
DE Human cytoskeleton-associated protein, CSAP-6 cDNA.
XX
XX Human; cytoskeleton-associated protein; CSAP-6; atherosclerosis; cancer;
XX gene therapy; gene; 88.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 276..4079
XX FT /*tag= a
XX FT /product= "Human CSAP-6"
XX FT sig_peptide 276..353
XX FT /*tag= d
XX FT sig_peptide 276..347
XX FT /*tag= b
XX FT mat_peptide 348..4076
XX FT /*tag= c
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XX FT mat_peptide 354..4076
XX FT /*tag= e
XX FT /product= "Human mature CSAP-6 protein"
XX
XX WO200279404-A2.
XX
XX 10-OCT-2002.
XX
XX 25-MAR-2002; 2002MO-US009288.
XX
XX 29-MAR-2001; 2001US-0280508P.
XX 03-APR-2001; 2001US-0281323P.
XX 13-APR-2001; 2001US-0283769P.
XX 04-MAY-2001; 2001US-0286099P.
XX 10-MAY-2001; 2001US-0290518P.
XX 18-MAY-2001; 2001US-0291870P.
XX 29-MAY-2001; 2001US-0294451P.
XX
XX (INCY-) INCYTE GENOMICS INC.
XX
XX Hafalia AJA, Tang TY, Yue H, Khan FA, Ison CH, Baughn MR,
XX Warren BA, Duggan BM, Thangavelu K, Honchelli CD, Azimzai Y,
XX Elliott VS, Burford N, Ding L, Yue H, Becha S, Emerling BM,
XX Richardson TW, Lee SY, Bandman O, Lai PG, Lee S, Gietzen KU,
XX Walla NK, Griffin JA, Lee EA, Swarnakar A, Ring HZ, Jones KA,
XX
XX WPI, 2003-092894/08.
XX
XX P-PSDB; AAB32108.
XX
XX New human cytoskeleton-associated proteins, useful for preparing a

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PT composition for diagnosing or treating a disease or condition associated
PT with decreased expression or overexpression of functional CSAP e.g.,
PT cancer.
PS Claim 5; Page 209-210; 233pp; English.
XX
XX The invention relates to new human cytoskeleton-associated protein (CSAP)
XX and its polypeptide. The polypeptide is useful for preparing a
XX composition for diagnosing or treating a disease or condition associated
XX with decreased expression or overexpression of functional CSAP e.g.,
XX atherosclerosis or cancer. The present sequence is human CSAP-6 cDNA. The
XX invention is useful in gene therapy
SQ Sequence 4080 BP; 987 A; 1241 C; 1117 G; 735 T; 0 U; 0 Other;
Query Match 18.8%; Score 778.2; DB 7; Length 4080;
Best Local Similarity 54.5%; Pred. No. 3.2e-218;
Matches 1700; Conservative 0; Mismatches 1388; Indels 29; Gaps 6;
Oy 167 CCTGATTTCTCTTCTGTCGAGATGATTAAGTACAGTGAAGTACCTTGTACCAAAAC 226
Db 313 CCTTCTCTCTGCTCTCTCTCTGAGTCTTGGGAGGACATGAAATTCATGATCCAGCA 372
Oy 227 TTTTGAAAGACTTGTGACAGCTTCCACCATCACCACAGTCTTCCAAAAGTTACATTA 286
Db 373 TTCAGAAATGAGCTGACGAGCGCCACCATCACCACAGTCCAGCAAGATCACATCG 432
Oy 287 TTGACCTTCGGAGAAATTTGTAATTCAGTGTGAAGCCAAAGGAAACCGCCCAAGT 346
Db 433 TGGACCCCGGTATTAACCTCTGATTAAGTGTGAAGCAAAAGGAAACCTTGCCTCAGCT 492
Oy 347 TTTCTGAGACCCGTATGAGGACTCATTTTGAATCATGATTAAGACCTCTGTACATGA 406
Db 493 TCCACTGAGCAAGAAACAGAGATTTCTTAACATGCGCAAGAACCCCGGGGTGCATGA 552
Oy 407 AGCTGGCACAGAAACGCTCATTAATTAATCATATGAGGAAAGGAAAGTGAAGACTTATG 466
Db 553 GGAGAGAGTCTGGGACCTTGATTAATTCAGTGTGCGGCGGCGGCGGAGTAATG 612
Oy 467 AAGAGTCTATGAGTACAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGT 526
Db 613 AAGGAGAAATGAGTCTGTCGCGCCCAAAATTTGGACCGGCTGTCTCAATAGATTC 672
Oy 527 TTGTCGCGCCATCCAGATCACCATTGTGAGCCCAAGAAACCTTGAACCAATCACACTTC 586
Db 673 GCTCGAGGTGTCTAAATCTCTCTGTGCGCCAAAGAAACCTTAACCTGTGCGTTC 732
Oy 587 AAGTGTGAGTCTTAAATCTCTCTGAGACCCCAATTTGATTAACCACTATTA 646
Db 733 AAGAGGCGCTCTTGAACGCTTCAGTGCACCCCGCTGACCTTCATCCCGGTCA 792
Oy 647 TATTTTGAATGATTAATCTCTTCAAGACCTTCAAAAGTGAAGAGTTCAGAGTT 706
Db 793 TCTTCTGATGAGACAGCTTCATGAGCCCATACCCAAAGATGTCTTCAAGGCCC 852
Oy 707 TGAATGGGACCTTATTTTCCAAATGTCCTCCAGAGGACACCCGCGAAGCTATATCT 766
Db 853 ATTAAGGAGACCTTAATCTTCCAAAGTGTCTGAGAGACATGAGACCGACTACAGTT 912
Oy 767 GTTATGCTAATTTAATCACTCAACCATACAGACAGAGCAACCTATTTTGTGAAG 826
Db 913 GTTAAGCCCGCTTCACTTCAACCATCACAGAGCAAGAAACCTTTCACCTTCAGG 972
Oy 827 TGATTTCAATGATTAATGATGACATATAGCTGTAAATTTGAGTGCACTGAGTTT 886
Db 973 TCTTCAACCAACACCTTATTAATGAC-----TGTCTTAAAGAAACCACTTGACATGT 1026
Oy 887 ATGAGTCTAATCAAGTAGAGAGAGGCAACAATTTTAACTCCAGAGGCAATGCA 946
Db 1027 ACAATGCCGAGAGAGTGAAGAAAGAACCAAGCTTCAATATCCAGGCGACCGGCA 1086
Oy 947 GTTAACAAAGAAATTAAGAGAAATGTGCTTTCAGCTGAGTGCATTCAGAGAGCTGC 1006

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Db 1087 GCAGCCAGATGCTGCTTGTGCGATGAGACCTCTGCTGTAATGATCGCTCCGGGTCC 1146
Qy 1007 CTACCCCAATTTATTTACTGGGCAAGAGATGGAATGCTACCCCAAAAAGAGACAGTTT 1066
Db 1147 CAACACCAACATCGATGCTACAGAAAGTGGGACCTCCCATCTGTAAGGCCAAGT 1206
Qy 1067 ATAGAACTTTGAGAAAACCTTGACAGATCAATCATGTTTCAAGAGACACTGGAATT 1126
Db 1207 TTGAGAACTTTAATAGGCCCTGCTATCAAAATGCTCTGAGAAAGCTCCGGGAGGT 1266
Qy 1127 ACCAATGTAATAGAAAAAATGCAATTAAGACCATCAACATACCATTTCTGTTAAGTTA 1186
Db 1267 ATTTGCGCTGCTCCCAACAGATGGGAGACATCGGACACAGATCTGGTGAAGTTA 1326
Qy 1187 AAGCGGCTCCATCTGATGATCAGCCCTCAAAAATGTTGCTGCTCCAGAGAGAGATG 1246
Db 1327 AAGCTGCTCTTAATGCTGAGCAACCAAGAACCTTAATTTGCTCTCGGAGAGATG 1386
Qy 1247 GGAACCTGATCTGACAGGCTAATGCAACCCCAAAACCAAAATTAAGCTGTTAACAAATG 1306
Db 1387 GGAAGACTGGTGTGTGAGCCAAATGAGAAACCCCAACCACTGTCAGTGGATGTAATG 1446
Qy 1307 GAGTCCCAATAGAAATTTGCCCTGATGACCCGACGCAAAAATAGTGGCATCAATTA 1366
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Qy 1427 ATGATATTTTACTGGCAAAACGATTTGTAATGCTGCTGACGACCAACGATCTCA 1486
Db 1567 ATGGCTACTGCTGGGCAACGCTTTGTGATGTGTGATGATGCGGCTCGGATGCTGT 1626
Qy 1487 CACCTGCAACACACTCTACAGGCTATTGCAAAACAGGCTGTTTACTAGACTGTGCT 1546
Db 1627 CCCCCGGAACGACTCATTCGAGTATTTTACCAACCGGACGCGGCTGACCTGCTT 1686
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Db 1866 GTCCGCTGAGGTCAAAAGACCCCAACAGATCTTACCGGATGCTCAGAGACAGAGTGGC 1925
Qy 1786 CAAAGGAGAGATGCTGCTTTGATGCAAAAGTGAATCATGATCAACCTTATCCCTC 1845
Db 1926 ABAAGGGGACCAACGCTGACGTGAGTGTCCGGTGAACGACCCCTCCCTGAAACCTC 1985
Qy 1846 ACTGTCCTGTGCTGAAGACCAACAGGAACTGCCAGATGTAAGTTCATCTGTTGAC 1905
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Qy 1906 AAGGATCATCTAGTGTAGTACATGTCATGACGATGACAGGCGGACCTTACAGTGTG 1965
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Qy 1966 GCCAACACCACTCTGAGACAGCTCTCCGCAAGGCTGTGCTTACGCTTTTCTCTACT 2025
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Qy 2131 AACATAGCCCCATTAACAAATTCATTCATTCGAAATGAAATGATCAATGACCAAGCAGG 2190
Db 2286 AACAAACCCCCATCAACAGACTACGTCCTCCAGTTTGAAGAACCAAGTTCACACCTGG 2345
Qy 2191 CTGTGGCAACCAAACTGAAGTTTCTGGAACAGACACAGAGCCAGCTGAAGCTGCT 2250
Db 2346 GTCTGCAATGACATTCACAGTACCCCGGACGCTTAATCAAGCTGCTCCGCTGTC 2405
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Qy 1727 GGAATAAATAGAGATGAGCAAAAGATGAATTC- ACTTAACAGCCCAATATGACTGTG 1785
Db 1600 GTCCGCTGAGAGTAAAGACCCCAACAGATCTACCGGATGCGGAGACAGATGTGCG 1659
Qy 1786 CAAGAGGAGAGATGTCTCTTTGAATGCAAGTGAACATGATCACCTTATCTCTC 1845
Db 1660 ABAAGGGGACCAAGTGCATGAGATGTGGGTGAAGACGACCCCTCTCTGAACCTT 1719
Qy 1846 ACTGTCTGTGCTTAAGACCAACAGGAACTGCCCATGATGAAGTGTACTGTATAC 1905
Db 1720 ACCGTCTACTGTGAAGATGACAGCGCTTATATTTGAAGAGATGAAGAGAA 1779
Qy 1906 AAGATCATCTAGTGTAGCTGATGTCAATGCAAGGAGAGCTTACAGTGTGTG 1965
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Qy 2386 TCAAGCTGATTAATTTGAATTAAGTGAAGCTTGAATGTTGAATCTTAATGAG 2445
Db 2230 ACCAGAAAGAACCAATGAGATCACTGTGACGCTCATGAAATGCCACTCGGCTTTGGC 2289
Qy 2446 CAGGCTTTCAGTACAAAGTTTATGCTGAGGCGCAAGAAATGATGATGAATGACATCT 2505
Db 2230 CCAACCTGCTCATATTTGATGAGAGGAGAGAGATCTGAGAGGCTTGAACAC 2349
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Db 2407 GAGATCCAGTCTCAGGCTGAAGATGATCTTGGGAAAGGCGCTGAGCCAGATCCGTATC 2466
Qy 2626 GGAATCTTGGAGAAAGACTGCCAAATGAGTGTCTCTGGAAGCGTGTGTAATGTGAG 2685
Db 2467 GTTATCTCGGAGAAATTAATCCAGGGCTGTGCGCCACTGAAGTTAAAGTCCGATCTATG 2526
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Qy 2746 CTACAGGCTATCGATTTACTATTGGAAGACCAAGTTCATCTTAAAGAAACAGAGT 2805
Db 2587 CTCAAGAGTACCGGCTACTACTGAGGAGAGAGACCTTGTGAAAGAACCTGTGGGTG 2646

QY 2806 CACATTGAGAAAAAGATCCCTCACTTCAAGGACAGACATCATGTCATGTCGGCCGGG 2865
 DB 2647 TCTCAGAAAGACAGACAGACAGACCTTCTCTGGAGACCGCTCCGTGGTGTCTCCGCC 2706
 QY 2866 CTAGAGACCCCTTTAGCCACTACACACATGATGTCGAGTGTCAATGGGAAAGGGAGGCG 2925
 DB 2707 CTCTTCCCTACAGTAATCAAGCTGAGATGTTGTGTCAATGGAGAGGTGATGGG 2766
 QY 2926 CCAGCCAGCCCTGACAGAGCTTTAATCTCCAGAGAGAGTCCCGACAGTCTCCGTGTCT 2985
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 DB 2887 CCAATATGGGATCATGTGATGATCACTTCAATATGTCGCTGTACGTTCTCCCAAGTT 2946
 QY 3104 -----AATTAGCCCTCTGTGATGTTGAAATTCCTGCAACAAAGACAGGTTG 3153
 DB 2947 AACGGGACCAAGTATGAGAAAGAGATAGTGAAGAACTTCTCTCCATGACCAAGTTTC 3006
 QY 3154 ACTTTAAAAAATTTAATTTAGACACTCGATATAGTTTATTTCTATGACAAACATCA 3213
 DB 3007 ACCGTTCAGAAAGACGAGACCCCGTGTACCGTTACCGTTTACCTCAGCGCCAGAGACG 3066
 QY 3214 GCAGATCAGAAAGTCAAAATTACAGAGAGAGTAAACAACCTGTGATGAAGCTGG 3269
 DB 3067 GTGGGCTCTGGGAGACCGCTACAGAGAGTACACCGACACCCCGAATGAAGTAG 3122

RESULT 13

AAK51848 ID AAK51848 standard; cDNA; 4739 BP.

AAK51848;

06-NOV-2001 (first entry)

Human polynucleotide SEQ ID NO 393.

Human: cytokine; cell proliferation; cell differentiation; gene therapy;

KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;

KM tissue growth factor; immunomodulatory; cancer; leukaemia;

KW nervous system disorder; arthritis; inflammation; ss.

OS Homo sapiens;

PN WO200157190-A2.

09-AUG-2001.

05-FEB-2001; 2001WO-US004098.

03-FEB-2000; 2000US-00496914.

20-JUN-2000; 2000US-00560875.

19-JUL-2000; 2000US-00620325.

01-SEP-2000; 2000US-00654936.

15-SEP-2000; 2000US-00663561.

20-OCT-2000; 2000US-00693325.

30-NOV-2000; 2000US-00728422.

(HYSE-) HYSEQ INC.

Tang YT, Liu C, Dirmnac RT, Asundi V, Zhou P, Xu C, Cao Y;

Ma Y, Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZM;

Xue AJ, Yang Y, Wejhtman T, Goodrich R;

WPI; 2001-476283/51.

DR P-SDB; AAM78715.

XX Nucleic acids encoding polypeptides with cytokine-like activities, useful
 PT in diagnosis and gene therapy.
 PS Claim 1; Page 1489-1493; 6221pp; English.
 CC The invention relates to polynucleotides (AAK51456-AAK53435) and the
 CC encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to
 CC cytokine, cell proliferation or cell differentiation or which may induce
 CC production of other cytokines in other cell populations. The
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, haematopoiesis regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and
 CC activ/inhibin activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
 CC inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111
 CC (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the
 CC sequence listing were missing at the time of publication
 XX

Sequence 4739 BP; 1171 A; 1357 C; 1301 G; 910 T; 0 U; 0 Other;

Query Match 17.0%; Score 702.4; DB 4; Length 4739;

Best Local Similarity 53.8%; Pred. No. 9,1e-196; Mismatches 1326; Indels 80; Gaps 6;

Matches 1638; Conservative 0;

242 TACAGCTTCACACATCAACCCAGCTCTCCAAAGATTATTAATTAACCTCGGAGAG 301

7 TCCGCGCCGACCAATCAACAGAGTACGAGAGATCAATCTGTGAGACCCCGTATTA 66

302 ATATTGTAATCCAGTGTGAAGCAAGGAAACGCGCCCAAGCTTTCTGAGACCGTGA 361

67 ACATCCTGATGAGTGTGAAGCAAAAGGAAACCTGCCCCAGCTTCACTGAGACAGAA 126

362 ATGGGATCATTTTGAATCAATCAATTAAGACCTCTGTGTGATCAATGAAGCTCGACAGAA 421

127 ACAGCAGATTTCTTAACAATCGCAAGGAAACCCCGGCTGTCAATGAGAGAGAGTGTGGA 186

422 CGCTCATATTAATCAATCAATGAGCAAGGAAAGTGAAGCTATGAAGAGTCTATCACT 481

187 CCTGTGTATTAATCAATCTTCCGAGTGTGCGGCGGCGGAGGAAATATGAGGAAATACAT 246

482 GTACAGCAAGAAAGCAAGCGGAGTGCAGTTTCTAATTAACATTTGTCGCCCATCA 541

247 GCTTGCGCCGCAAAATTTGCGACGCGCTGTCAATGATGATCGCGTGCAGTGTCTA 306

542 GATCAACATTTGTGAGCAAGAAAGAACTTGAACCAATCACTTCAAGTGTCACTGT 601

307 AATCTCTCTGTGTGCGCAAGGAAACCTAAGACCTGTGTGTGTCAAGAGGCGCTCTT 366

602 TAGTACTTCCCTGAGAGACCCCAATTTGATTAACCACTTAATTTATTTGATGATGA 661

367 TGAAGCTCAAGTGCAGAACCCCGCTGTGATCTTCACTCCCGGTCACTTGTGATGAGAG 426

662 ATTCCTTTCAAGACTTCCCAAGAGTGAAGATTTCTCAAGTTTGAATGGGACCTTT 721

427 GCTCATGAGGCCATCAACCAAGCAAAAGTGTCTTCAAGGCGCATTAACGAGAGACTAT 486

722 ATTTTTCATATCTCTCCAGAGAGACCCCGGAGAGATATATCTGTATATGTAATTTA 781

487 ACTTCTCCAAAGTATGTCGAGAGATGAGACACGACATCAAGTTGTAAGCGCCCTTCC 546

782 ATCATACTCAACATCAACAGAGAGCAACTATTTCTGTGAAGTGTGATTTCAAGTGA 841

547 ACTTCAACCAACATCAACAGAGAGCAACTTTTCACTTCAAGTGTGATTTCAAGTGA 901

842 AATTGAATGACACTAAGTGTGATTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 901

607 GAGT----- 610

902 GTAGAGAGAGGCGACCAACATTTTAACTTCCAGAAAGCAATGCAATGAAGAGAGAT 961

611 -TGCAAGAAAGAACACCAAGCTTCAATGATATCCAGAGGACCGCGAGACCGCAGATGTGC 669

QY 962 TAAAGAAATGTCTTTCACTGAGTCAATGACAGAGACTGCCATACCCCAATATTTT 1021
DB 670 TTGCTGGACATGACCTCTGCTGGAAATGATGCGCTCCGGGGTCCCAACACAGACATCG 729
QY 1022 ACTGGCAAGAAAGATGGAATGCTACCAAAAACAGACAGTTTATAGAACTTTGAGA 1081
DB 730 CATGTACAGAAAGGAGGGGAGCTCCCATCTGATAGGCCAAGTTTGAACCTTTAATA 789
QY 1082 AAACCTTGACATCTTCACTGTTTCAAGACAGACTCTGAAATATACCAATGATAGCA 1141
DB 790 AGGCTGCTGCTATCACAAATGTCTGAGGAAAGCTCCGGGAGTATTTCTGCTGGCTT 849
QY 1142 AAATGATTAAGAGGAGCCATCACCATATCTTCTGTTAGAGTTAAAGGGCTCCATCT 1201
DB 850 CCAACAAAGATGGGACAGATCCGGACACGATCTCGGTGAGATGAAGGCTGCTCCCTACT 909
QY 1202 GATTCACAGCCCTCAAAATCTTGTGTGTCTCCAGAGAGATGGGACCTTGATCTGCA 1261
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QY 1322 TTGCCCCGATGACCCAGAGAAAATAGATGAGCATACCTATTTTTCATTAATGTTT 1381
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QY 1382 AAGAAAGATCAAGTGAATATCACTGATCAATGCTCTTAATGAATATGATTTTATCTG 1441
DB 1090 AGATCAGACAGAGGCTGTGTGTACAGTGAACACCTCAAGACAGATGGCTACTGCTGTG 1149
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QY 1622 TTTTATGATGAATGGAATCTTTGGAATCAAGATCTTACATGATCTTTAAAGAAATTC 1681
DB 1330 ATGTTATGAGAACGCGAGCTGGAAT-TAAGATATCGCAAAAGAGCCAGGCGATC 1388
QY 1682 CTGTGCGCAAAAGACAGTACAGAACTTATCGTGTGTGCAAGAAATTAATTAGGA 1741
DB 1389 TACACTGTGTGTGCGCAACATCTGGGCAAGCTGAAAACCAATCTCGCTGTGAGTCT 1448
QY 1742 TGGCAAAAGATGAAATTC-ACCTTACAGCCGGAATATGAGTTGTGCAAGAGGAGCATG 1800
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QY 1801 GTGTCTTTGAATGCAAGTGAACATGATCACACTTATCTCTCACTGTCTGTGGCTG 1860
DB 1509 GTGCAAGCTGAGTGTGGGTGAAGACAGCCCTCCCTGAACCTCACTCTCTGTGGCTG 1568
QY 1861 AAGGACAAAGGGAATGCGCCAGTATGAAGTTTCACTGTGCAAGAGATCATCTAGTG 1920
DB 1569 AAGGATGAGAGCCCTCTTATATTGAAACAGATTAAGAGAGAGACAGATTTCTGTACC 1628
QY 1921 GTAGCTGATGTCAAGTACAGATGACAGGAGACTTACAGTGTGTGCAACACACTGTG 1980
DB 1629 ATCTTTGGGTGGCAAGAGGAGACAGGAGAGTTTACAGTGTGTGCGACAGACAGCTTA 1688
QY 1981 GACAGGTCTCGCCAGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2040
DB 1689 GACCAAGACTGTGCGCAAGGCTTACCTCACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1748

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QY 2086 CAACTTGAAGAAATGTTTCACTGTGTATGAGACCCAGGAGATGACAAATATGCCCTATT 2145
DB 1809 CTGGCCGAGAGAGGCTGTGGGTGAGCTGTGATCTCCCGGAGATGCTTAACACAGCCCATC 1868
QY 2146 ACAAAATCATCATGATATGAAATGCAATGACCAAGCCAGGGCTGTGGACCAAC 2205
DB 1869 ACAGACTTACGTGTCTCAAGTTTGAAGAACAGTTTCAACTGGGGTCTGGACATGACAT 1928
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DB 1929 TCCAAATACCCCGGACGCTTAACTACGCGCTCTCCGGCTGTCCCGATGTCAACTAC 1988
QY 2266 TCCCTTCCGCTGATGAGTGAACAGATTTGGAGAGCTTGGCCAGAGCGTCTGAG 2325
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QY 2386 TCAGAGCTGATTAATTTGAGATTAAGTGAAGCCCTTGAATGATTTTCAATCTAATG 2445
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QY 2446 CAGGCTTTCAGTCAAAAGTTAGCTGGCGCCAGAAAGATGTGATGATGATGACATCT 2505
DB 2169 CCCAAGCTGCTGCTACCTTGTCAAGTGAAGGCGGAGAGACATGAGAGCTGGAACAAC 2228
QY 2506 GTGTGTGGCAATATTAATCAAAATATATGTCTCAGGACCCCACTTTGTCCATAC 2565
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QY 2346 GGTACTCCGAGGAAGATATATCCAGGGCTGGCCCACTGAAGTTAAATCCGAGTATG 2405
QY 2686 AACAGTACTTACGCGAGGTGACGTGGAGCCAGTACCTCTGAAGAAAGATCCGAGAGAC 2745
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DB 2526 TCTCAGAAAGACAGAGAGCAGCTTCCCTGTGACCGCTCTCGTGGGTGTGTCTCGC 2585
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DB 1210 TCATTCGATGTATCTTTTCAACCGGACCGGCTGAGCTGCCCTTCTTGGGTCTCCCA 1269
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DB 1569 AAGGATGACGAGCCGCTATATTTGAAACAGGATGAAGAGAAACATTTCCGAC 1628
QY 1921 GATAGTATGATGATGACATGACAGCGGGAACCTAAGTGTGTGCGCAACCACTGTG 1980
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QY 2041 GTTTACGATGTCCCAATCTCTCTTTGAATTGAACATGACAGATCACTTGAACAAAGT 2100
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QY 2101 GTTACGCTGTATGACATGACAGCGGATGACAAATAGCCCATTTACAAATTCATATC 2160
DB 1779 GTGCGCTGTACCTGATCTCCGCGGATGCTTAAACAGCCCATCAACATCACTGCTGC 1838
QY 2161 GAATATGAAGATGACATGACAGCGGCTGTGACCAACCAACTGAAGTTTGTGA 2220
DB 1839 CAGTTTGAAGAAAGACAGTTTCACTGAGGCTGTGACATGACATTTCCAAAGTACCCGAG 1898
QY 2221 ACACAGACCAAGCCAGCTGAAGTGTCTCTTACGTAACATCTCTTCCGCGTATG 2280
DB 1899 ACGCTTAACTACGCGCTCTCCGCGTGTCCCGATGATCACTACAGATTCGCTGCTAT 1958
QY 2281 GGAATGAAGATGAGTGGGAAAGCTTGCACAGCGAGGCTGTGAGAGATTTTGAAGAA 2340
DB 1959 GGCATTCAGAGGTTGGAGAGCAACCCACCTCTCCATTCGAGGCTTACCGAAGCAAT 2018
QY 2341 GCCTAGAAACAGATTAACCAACCCACAGCTGTGAAAGATGAGGATCAGAGCTGATAT 2400

DB 2019 GGAGCAACCCCGAGTCCAAATCTGTATGACGTGAAGGGAGAGGAGACCAAGAAACAC 2078
QY 2401 TTGGAATTAAGTGAAGCCCTTGAATGTTTGAATCAATGAGGCGAGCCCTGATAC 2460
DB 2079 ATGAGATCACTGAGCGCCCAATGATGACCTGCGCTTTGGCCCAACTGCGCTAC 2138
QY 2461 AAGTTAGCTGCGCAGAAAGATGATGATGATGATGATGATGATGATGATGATGATG 2520
DB 2139 ATTGTCAATGAGGCGGAGAGAGATCGAAGGCGCTGGAACAAAGTCAAGT---TGG 2195
QY 2521 GTATCCAAATATATGTCTCAGGACAGCCCACTTTGTTCATACCTGATCAAGTTGAC 2580
DB 2196 GGCCTCTGCTAGTGTGTGGGAGAGACCCAGCTACGTGCTGCTATGAGATCCGATCCAG 2255
QY 2581 GGCCTGATGATGATGAGGTTTGGCCCGAGCGAGCTGATGATGATGATGATGATGATG 2640
DB 2256 GCTGAATATGATGATGAGGAGGCGCTGAGCCAGAGTCTGATGATGATGATGATGATG 2315
QY 2641 GACTCCCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2700
DB 2316 GATTAATCCAGGCTGCGCCCACTGAATTAAGTCCAGTATGATGATGATGATGATGATG 2375
QY 2701 GAGTGCATGAGGACCACTGATCTGTAAGACATCCAGACACCTTACAGGCTATGCG 2760
DB 2376 AGCTTCAATGAGACCGGCTTACTCCGACAGGTCAGGCGCAGCTCAGAGATACGA 2435
QY 2761 ATTATATATGAGAACCAAGTCTATTAATAAAGACATGATGATGATGATGATGATG 2820
DB 2436 GCTTACTATGAGGAGAGAGAGCTTGTGAAGAACTGTGTGTGTCTTGAAGAGACAG 2495
QY 2821 ATCTTCACTTCAAGGAGAGAGAGATGATGATGATGATGATGATGATGATGATGATG 2880
DB 2496 CAAGCAGCTTCTCTGTGATCCGCTCGGTGCGGTGTGTGTGTGTGTGTGTGTGTGT 2555
QY 2881 CACTACACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2940
DB 2556 AACTACAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2615
QY 2941 AGAGCTTATATCTCCAGAGAGATGATGATGATGATGATGATGATGATGATGATGAT 3000
DB 2616 AAGAGTTCACCAACCGGAGAGAGATGATGATGATGATGATGATGATGATGATGATG 2675
QY 3001 CCAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3060
DB 2676 CCAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2735
QY 3061 ACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3120
DB 2736 ATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2792
QY 3121 GATTTGAATATCTGCGCAAGACAGTGTGATTTAAATAATTTAAATTTTACGACT 3180
DB 2793 GTGGAATATCTCTCCCAATGATGATGATGATGATGATGATGATGATGATGATG 2852
QY 3181 CGATTAATGATTTATTTTATGACAAACATGATGATGATGATGATGATGATGATGATG 3240
DB 2853 GGTACCGCTTATCTTCAAGCGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2912
QY 3241 GAAGCAGTAACTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 3269
DB 2913 GAGTCAACAGACCCCGAATGAAAGTNG 2941

RESULT 15
ADB61924
ID ADB61924 standard; cDNA; 2462 BP.
XX
AC ADB61924;
XX
DT 04-DEC-2003 (first entry)
XX
DE Human cDNA encoding clone BNGH42007798.

[illegible][illegible]

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 QY 1367 TTTTTCAAATGTCAAAGAAAGTCAAGTGCATATATCATGCAATGCTCTAATGAAT 1426
 Db 1468 TCTTCGGGACACCCAGATCAGCAGAGGCTGTGTACAGTGCACACCTTCCAGAGC 1527
 QY 1427 ATGATATTTTACTGCGAAACGATTTGTAAATGTCGCTGAGCCACACGAAATCTCA 1486
 Db 1528 ATGGCTACTGCTGGCCAAACGCTTTGTAGTGTGCTGATGTGCGCCTCGGATGCTGT 1587
 QY 1487 CACCTGCACAAACACCTTACAGAGTATTCGAAACAGGCTGTTTACTAGACTGCTCT 1546
 Db 1588 CGCCCCGGACAGCTCATTCAGTGAATCTTTACAAACGAGACGCGCTGAGACTGCCCC 1647
 QY 1547 TCTTTGGGTCTCCTCTCCCAACATGAGTGTGTTAAAGAGCTAAAGAAAGTCTCTTC 1606
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 QY 1607 ATGAAGATATTTATGTTTACATGAATGAACCTTTGAAATCAAAGATGCTACATGA 1666
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 QY 1786 CAAAGAGGAGCATGTGTCTTTGAATGCAAAGTGAAACATGATCACACTTATCCCTC 1845
 Db 1887 AGAAGGGGACACACGCTGACAGTGTGCGGTGAACACGACCCCTCCGAAACTC 1946
 QY 1846 ACTGTCTGTGCTGAAGACAAACAGGAACTGCCCATGATGAAGTTCACTGTTCAC 1905
 Db 1947 ACCGTCTCTGTGCTGAAGATGACGACCGCTCTATATGTGAACAGATGAAGAGAA 2006
 QY 1906 AAGGATCATCTAGTGTAGTGTAGTGTCAATGTCAGTGAAGATGACAGGGGACCTACACGTGTGTG 1965
 Db 2007 GACGACTCCTGACCATCTTTGGGGTGGCAGAGCGGACAGGGCAGTTACACGTGTGTG 2066
 QY 1966 GCCAACACCACTGTGACAGCGTCTCCGACAGGCTGTGCTTAGCGTGTGTCTCTACT 2025
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 QY 2026 CCAACTCCAGCTCCGTTTACATGTCCCAATCTCTCC 2064
 Db 2127 CCATGCTCACCTGGCACTGACCAAGCCCACTCCCTCC 2165

Search completed: May 22, 2004, 22:32:06
 Job time : 1621 secs

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OM nucleic - nucleic search, using sw model

Run on: May 22, 2004, 20:16:01 ; Search time 15573 Seconds
(without arguments)

11505.818 Million cell updates/sec

Title: US-09-301-380-1

Sequence: 1 cttcaagttccccgcata.....tggtagagagtatatcttc 4134

Scoring table: IDENTITY_NUC

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

1:	gb_da:*
2:	gb_hhg:*
3:	gb_in:*
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5:	gb_ov:*
6:	gb_pat:*
7:	gb_ph:*
8:	gb_pl:*
9:	gb_pr:*
10:	gb_ro:*
11:	gb_sts:*
12:	gb_sy:*
13:	gb_un:*
14:	gb_vt:*
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32:	em_hhg_inv:*
33:	em_hhg_other:*
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36:	em_hhg_rtd:*
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38:	em_hhg_vit:*
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41:	em_hhg_other:*

Pred. No. is the number of results predicted by chance to have a

Result No.	Score	Match	Length	ID	Description
1	4134	100.0	4134	9	HSU55258
2	3751.6	90.7	3997	6	AB7637
3	3727.6	90.2	3900	6	HSC7NRCAM
4	3316	80.2	6254	6	AX099489
5	3316	80.2	6254	6	BD190781
6	3245.6	78.5	6240	9	HSMB06153
7	3233.6	78.2	6218	9	AB002341
8	2895.2	70.0	4486	10	MM0543321
9	2551.8	61.7	4044	10	RNDB1037
10	2549.6	61.7	4944	10	BC055053
11	2468.4	59.7	5608	10	AK122252
12	2245.8	54.3	3942	5	CHKBV0
13	2236	54.1	3943	5	GNBRAM
14	2236	54.1	3943	6	ARI177825
15	863	20.9	4041	5	GCNE04FAC
16	740.6	17.9	3498	10	RNDB1035
17	730.8	17.7	3752	10	AY061639
18	703.2	17.0	5822	10	RATNKRIND
19	689.6	16.7	5071	10	AK129207
20	617.4	14.9	4465	10	MM0543322
21	588.6	14.2	4955	9	AB018299
22	586.2	14.2	3651	10	RNDB1036
23	551.6	13.3	2692	9	AK099330
24	525.6	12.7	557	9	AF462608
25	472.8	11.4	7642	9	AX818174
26	472.8	11.4	7642	9	AF002246
27	445.4	10.8	2462	6	AX746553
28	445.4	10.8	2462	9	AK090639
29	441	10.7	2313	9	AK097802
30	436.4	10.6	975	10	BC060532
31	414.8	10.0	3960	9	AK126878
32	405.8	9.8	3783	6	ARI77819
33	405.8	9.8	3783	10	MMNCAM1
34	405.4	9.8	5093	10	RNNCAM1
35	401	9.7	5038	10	BC056988
36	386.4	9.3	4437	10	MM1L
37	359	8.7	4023	9	AF129167
38	358.6	8.7	416	6	BD05351
39	353.8	8.6	3768	6	AB102654
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43	351	8.5	3774	6	AR081015
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					AB7637 Sequence 1
					AF001057 Homo sapi
					AX099489 Sequence
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					BX538010 Homo sapi
					AB002341 Human mRN
					AJ543321 Mus muscu
					U81037 Rattus norv
					BC055053 Mus muscu
					AK122252 Mus muscu
					L08960 Chicken cel
					X58482 Chicken mRN
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					AS5224 G.gallus mR
					U81035 Rattus norv
					AY061639 Rattus no
					L11002 Rat ankryrin
					AK129207 Mus muscu
					AJ543322 Mus muscu
					AB018299 Homo sapi
					U81036 Rattus norv
					AK092330 Homo sapi
					AF462608 Macaca mu
					AX818174 Sequence
					AF002246 Homo sapi
					AX746553 Sequence
					AK090639 Homo sapi
					AK097802 Homo sapi
					BC060532 Mus muscu
					AK126878 Homo sapi
					ARI77819 Sequence
					X12875 Mouse mRNA
					X59149 Rat mRNA fo
					BC056988 Mus muscu
					X94310 M.musculus
					AF129167 Chloroceeb
					BD05351 Secreted
					AB102654 Pan trogl
					AB102653 Homo sapi

ALIGNMENTS

RESULT 1					
LOCUS	HSU5258		4134 bp	DNA	linear
DEFINITION	Human HBRVAVO/Nr-CAM precursor (HBRVAVO/Nr-CAM) gene, complete cds.				
ACCESSION	U5258				
VERSION	U5258.1				
KEYWORDS	GI:1621282				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
REFERENCE	1 (bases 1 to 4134)				
AUTHORS	lane, R.P., Chen, X.N., Yamakawa, K., Vielmetter, J., Korenberg, J. R. and Dreyer, W. J.				
TITLE	Characterization of a highly conserved human homolog to the chicken				


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 ACCESSION A87637
 VERSION A87637.1 GI:6736275
 KEYWORDS
 SOURCE
 ORGANISM
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 unclassified
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 AUTHORS Wang, B. and Kenwright, S. J.
 TITLE NEURAL CELL ADHESION MOLECULE SPLICING VARIANTS
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 DB 6 GTAAATTCGCTATGCAAGCTTAAATATGCGGAAAGAAAGCGCTTATCTGCGGACGA 65
 QY 163 GTGCCCTGATCTCTCTGTCAGAGATGATTAAGTCACTGGAAGTACTCTTATGCA 222
 DB 66 GTGCCCTGATCTCTCTGTCAGAGATGATTAAGTCACTGGAAGTACTCTTATGCA 125
 QY 223 AAACCTTTGAAGACTTGTATGAGCTCCACATCAACCAACAGTCTCAAAAGATTAC 282
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Qy	643	ATAATATTTTGGATGTATATTCCTTTCAAGACTTCCAAAGTGAAGAGTTTCTCA	702
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Qy	1423	GAAATATGATATTTACTGTGCAAAAGCATTTGTAAATGTGTGTGACGACCAACAGAAATC	1482
Db	1326	GAAATATGATATTTACTGTGCAAAAGCATTTGTAAATGTGTGTGACGACCAACAGAAATC	1385
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OY	1723	GCAGGAATTAATTAGGATGGCAAGATGAATTCATCTT-----	1763
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OY	1764	-----ACAGCCCGAATATGCAATGTTGCAAGAGGAGCATGTCCTTTGAA	1812
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 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

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 Homo sapiens (human)
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REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 MEDLINE
 PUBMED
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL

1 Wang, B., Williams, H., Du, J.S., Terrett, J. and Kenwright, S.
 Alternative splicing of human NRCAM in neural and nonneural tissues
 Mol. Cell. Neurosci. 10 (5-6), 287-295 (1998)
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 2 (bases 1 to 3900)
 Wang, B.
 Direct Submission
 Submitted (10-AUG-1997) Wang B., Department of Medicine, University
 of Cambridge, Addenbrooke's Hospital, PObox 157, Hills Road,
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FEATURES
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ORIGIN

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VERSION AX099489.1 GI:13538577
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SOURCE Homo sapiens (human)

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 AUTHORS Jacobs, K., McCoy, J.M., Lavalie, E.R., Collins-Racie, L.A., Evans, C.,
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AUTHORS   Weses, H. W., Weil, B., Amid, C., Oesinger, A., Podo, G., Han, M. and
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          This clone (DKFZp686L0246) is available at the RZPD in Berlin.
          Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
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ORIGIN

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Query Match      78.5%; Score 3245.6; DB 9; Length 6240;
Best Local Similarity 89.5%; Pred. No. 0;
Matches 3727; Conservative 0; Mismatches 14; Indels 423; Gaps 5;

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 REFERENCE
 AUTHORS
 TITLE
 Nagesse, T., Ishikawa, K., Nakajima, D., Ohira, M., Seki, N., Miyajima, N., Tanaka, A., Kocani, H., Nomura, N., and Ohara, O.
 Prediction of the coding sequences of unidentified human genes. VII. The complete sequences of 100 new cDNA clones from brain which can code for large proteins in vitro
 JOURNAL
 DNA Res. 4 (2), 141-150 (1997)
 MEDLINE
 97349984
 PUBMED
 9205841
 REFERENCE
 AUTHORS
 TITLE
 Ohara, O., Nagesse, T., Kikuno, R., and Nomura, N.
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 Submitted (28-MAR-1997) Osamu Ohara, Kazusa DNA Research Institute; 1532-3, Yama, Kisarazu, Chiba 292-0812, Japan
 (E-mail:cdna@fokkazusa.or.jp, Tel:+81-438-52-3913)
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ORIGIN

Query Match 78.2%; Score 3233.6; DB 9; Length 6218;

Best Local Similarity 89.4%; Pred. No. 0;

Matches 3722; Conservative 0; Mismatches 9; Indels 433; Gaps 5;

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QY	2251	CCTTACGTGAACACTACTCTTCCGCGGTGATGGCAGATGAAACAGATTGGGAAGACTTGGCC	231.0
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QY	3751	CAGGCTTATGAAAGGAATGATATGGGACATTTGGAAATATACAGTGTATGCAAGAACCAAG	3810
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 VERSION AJ543321.1 GI:29466305
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 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE
 AUTHORS Dirke, P., Montag-Sallaz, M. and Montag, D.
 TITLE Expression patterns of Li-family cell recognition molecules Ll,
 JOURNAL CHL1, Nrcam, and neurofascin in the mouse brain
 AUTHORS 2 (bases 1 to 4486)
 UNPUBLISHED
 REFERENCE
 AUTHORS Dirke, P.
 TITLE Direct Submission
 JOURNAL Submitted (06-FEB-2003) Dirke P., Neurogenetik, Leibniz-Institut,
 Breneckestr. 6, 39118 Magdeburg, GERMANY
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OY	1140	AAAAATSCATTTAGAGCGCATCCACCATACATTTCTGTTAGAGTTAAAGCGGCTCATYA	1199
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OY	1200	CTGATTCACAGCCCTCAAAATCTTGTGTGTCTGCCAGAGAGATGGGACTTGATCTG	1258
Db	1512	CTGATTCGTGGACCTCAAAACCTGTGCTTCCCGGAGAGAAATGGGACCTTCATCTG	1571
OY	1260	CAGAGCTAATGGCAACCCCAAAACCGAATTAGCTGTGTTAACAATGAGTCCCAATGA	1319
Db	1572	CAGAGCTAATGGCAACCCGAAACCGAATTAGCTGTGTTAACAATGAGTCCCAATGA	1631
OY	1320	AATTGCCCCCTGATGACCCCGACAGAAAAATAGATGGCATACCATATTTTTCAAATGT	1379
Db	1632	AATTGCTCTCATGACCCCGAGAGAAATAGATGGCATACCATATATTTTCAAATGT	1691
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OY	1560	TCCTCCCAACCATCGAGTGTTTAAAGAGCTAAAGAAAGTCTCTTCATGAAATATTTA	1619
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 VERSION U81037.1 GI:1842430
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 ORGANISM Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.
 REFERENCE 1 (bases 1 to 4044)
 AUTHORS Davis, J.O., Lambert, S. and Bennett, V.
 TITLE Molecular composition of the node of Ranvier: identification of
 ankyrin-binding cell adhesion molecules neurofascin (mucin+/chird
 FNIII domain-) and NrCam at nodal axon segments
 J. Cell Biol. 135 (5), 1355-1367 (1996)
 JOURNAL 97103184
 MEDLINE 8947556
 PUBMED 8947556
 REFERENCE 2 (bases 1 to 4044)
 AUTHORS Davis, J.O., Lambert, S. and Bennett, V.
 TITLE Direct Submission
 JOURNAL Submitted (05-DEC-1996) Howard Hughes Medical Institute, Duke
 University, PO Box 3892, Durham 27710, USA
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 ORGANISM
 Mus musculus (house mouse)

REFERENCE
 AUTHORS
 Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shellen, C.M., Schuler, G.D., Altshuler, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Frange, C., Raha, S.S., Logucliano, N.A., Peters, G.J., Abramson, R.D., Mulhany, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hilyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Sanchez, A., Whitting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakeley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,

TITLE	Butterfield, V.S., Krzywinski, M.I., Skalska, U., Smalins, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A. Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
MEDLINE	22388257
PUBMED	12477932
REFERENCE	2 (bases 1 to 4944)
AUTHORS	Strausberg, R.
TITLE	Direct Submission
JOURNAL	Submitted (11-JUL-2003) National Institutes of Health, Mammalian

USA 11/11/2011

COMMENT: Contact: MGC help desk

Email: cgabbs-remail.nih.gov
Tissue Procurement: The Cepko Laboratory
cDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland
Web site: <http://www.nisc.nih.gov/>
Contact: nisc.mcgc@hgrl.nih.gov
Akhter, N., Ayala, K., Beckstrom-Sternberg, S.M., Benjamin, B.,
Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,
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Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Latic, P., Legaspi, R.,
Maduro, Q.L., Mastello, C., Maekker, B., Mastrian, S.D., McCloskey, J.C.,
McDowell, J., Pearson, R., Startsrup, S., Thomas, P.J., Touchman, J.W.,
Turse, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L.,
Young, A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: <http://image.llnl.gov>
Series: IRAK Plate: 116 Row: 1 Column: 12.

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Location/Qualifiers

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 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE
 AUTHORS
 1 Okazaki, N., Kikuno, R., Ohara, R., Inamoto, S., Aizawa, H., Yuasa, S.,
 Nakajima, D., Nagase, T., Ohara, O. and Koga, H.
 Prediction of the coding sequences of mouse homologues of KIAA
 gene: II. The complete nucleotide sequences of 400 mouse
 KIAA-homologous cDNAs identified by screening of terminal sequences
 of cDNA clones randomly sampled from size-fractionated libraries
 DNA Res. 10, 35-48 (2003)
 REFERENCE
 AUTHORS
 2 (bases 1 to 5608)
 Okazaki, N., Kikuno, R., Nagase, T., Ohara, O. and Koga, H.
 JOURNAL
 Direct Submission
 Submitted (07-FEB-2003) Hisashi Koga, Kazusa DNA Research
 Institute, Laboratory for Genome Informatics, 2-6-7
 Kazusa-kamatori, Kisarazu, Chiba 292-0818, Japan
 (E-mail: mouse@kazusa.or.jp, Tel: 81-438-52-3919, Fax: 81-438-52-3918)
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ORIGIN

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 REFERENCE 1 (bases 1 to 3942)
 AUTHORS Kayem, J.F., Roman, J.M., de la Rosa, E.J., Schwarz, U. and Dreyer, W.J.
 TITLE Bravo/Nr-CAM is closely related to the cell adhesion molecules L1 and Ng-CAM and has a similar heterodimer structure
 JOURNAL J. Cell Biol. 118 (5), 1259-1270 (1992)
 MEDLINE 92381110
 PUBMED 1512296
 COMMENT Original source text: Gallus gallus (strain White Leghorn, sub_species domesticus) 17 day embryo cerebellum cDNA to mRNA.
 FEATURES
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 /strain="White Leghorn"
 /sub_species="domesticus"
 /db_xref="taxon:9031"
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 /dev_stage="17 day embryo"
 /note="putative alternatively spliced regions: AS10(aa. 588..597), AS12(aa.1003..1014), AS93/NTII#5(aa.1015..1107), AS CYT2(aa.1178..1181); immunoglobulin-like domains I-VI (aa. 1..586), fibronectin type III repeats 1-5 (aa.598..1002), transmembrane domain (aa. 1120-1142)"
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ORIGIN

Query Match 54.3%; Score 2245.8; DB 5; Length 3942;
 Best Local Similarity 75.0%; Pred. No. 0;
 Matches 2920; Conservative 0; Mismatches 842; Indels 129; Gaps 4;

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OY	218	ATCCAAAACCTTCTTGAAAGCTTGGTATACAGCCCTCAACCATCAACCCAAAGTCTCCAAAG	277
Db	121	ATTCAAAACCTTCTAGAAAGATTTGTCTCAACCTTCAACAAATATCTCAGCAGTCTCCAAAG	180
OY	278	ATTACATTATTGACCTCTGGGAGAAATATTGTATATCAAGTGTGAAGCCAAAGGAAACCCG	337
Db	181	ATTACATTGTGACCTCGAGAGAAATATTGTATATCAATGTGTAAACAAAGGAAACCAAC	240
OY	338	CCCCAAGCTTTCCGTGACCCCGTAAATGGAGCTCATTTTGACATGATATAAAGCCCTCTGG	397
Db	241	CTCTAGCTTCTCTCGAGCGCAATGGAACTCATTTTGTATATATATTAAGATGACAGG	300
OY	398	TCACCATGAAGCCTTGSCACAGGAACGCTCATATTAATCATCATGAGCCAAAGGAAAGCTG	457
Db	301	TACACATGAACCAATTCAGGAACCTTGTGTAAATATTTATGAAATGTGTGAAGGAGC	360
OY	458	AGACCTATGAAGAGTCTATCATGTTGACAGCAAGGAACGAACGCGAGCTGCAGTTTCTA	517
Db	361	AAGCATATGAAGAGTATATACAGTGTACAGCAAGAAATGAAGAAGACAGCAGCATTTTCA	420
OY	518	ATTAATATTGTTGTCGCCCCATTCACATCAACATTGTGTGACCAAAABAAAACTTGAACCA	577
Db	421	ACAAATATTGTATATACGGCCATCTTATATCCCTTTGTGTGACTTAAABAAAACTTGAACCA	480
OY	578	TCACACTTCAAAAGTGTGATCTTATAGTACTTCCGTGAGACCCCAATTTGGATTACAC	637
Db	481	ATCATAGTTCGAAGAGTGTATTCCTCTAGTACTTAACTGCAGACCTCTGTGGCTTACAC	540
OY	638	CACCTATATATTTTGGATGTATATTCCTTTCAABAGCTTTCACAAAGTGAAGAGATT	697
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OY	698	CTCAAGCTTTGAATGGGACCTTTATTTTCCAAATGTCTCCCAAGAGACCCGCGAAG	757
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OY	758	ACTATATCTGTATGCTAGTATTTATTCATACCTCAACCATTCAGAGAAAGCAACCTATTT	817
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OY	1058	GGACAGTTTATPAGACTTTTGAAGAAACCTTGCAGATCATTTCAATTTTCAGAGACAGCT	1117
Db	904	GAACTTTTTTTTGAAGAAATTTTAAAGAAACCTTCAAGATTAATGACGCTCTGAAAGTCACT	963
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Db	1024	TAACTGTAAAGCTGCCCCCATATCTGTATACAGACCCAGGAACCTTATATATTTGTCTCTG	1083
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Db	1144	TAACAAAATGGCGTTCCCATAGCAATTCGCCAGAAAGATCTTAGCAAGAAAGGTAGATGGGG	1203
Oy	1358	ATACCATTTATTTTTCAAATGCTTAAAGAAAGATCAATGACAGTATATTCAGTGCATAGCTT	1417
Db	1204	ATACCATTATTTTCTCAGCTGTGGAAAGCGGTAAAGTGGTGTATATTCAGTGAATGCTT	1263
Oy	1418	CTAATGAAATATGATGATTTTACTGTGGCAACGCAATTTGTAAATGCTGGCTAGCAACAC	1477
Db	1264	CTAATGATATGATTACTTGCTGGCAATGCAATTTGTGAATGTTCTTGCTAGCCACCA	1323
Oy	1478	GAATCCTCACACTGCAACACACTCTACAGCTCATTTGCAACAGGCTGCTTTACTAG	1537
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Db	1384	ACTGTGCTTATTTTGGTTCACCTTAAGCTGAAATCGAATGGTTTAAAGGGAGTGAAGGTA	1443
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Db	1444	GCATCTTGCAGGAAATGAAATATGTTTTCCATGATTAATGGAACCTTGGAAATTCOAAGTG	1503
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Db	1624	AAGTATTTCAAGAGTCTGCCCAAGCTTCAATTTGATGTATTAACCATGATCTTACCT	1683
Oy	1838	TATCCCTCACTGTCTGTGCTGCTGAAGACAACAGGGAATCTGCCAGATGTAAGTATCA	1897
Db	1684	TAAATCCAAAGTTATATGCTGTAAGAAACATATATGAATCTACAGATGATGAAGTTTC	1743
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Db	1744	TAGTTGGTAAAGACAACTTGACCATTAATGATGTAATCTGATTAAGATGATGAACATATA	1803
Oy	1958	CGTGTGTGGCAACACACACTCTGGAACGCTCTCCGACAGCGCTGTGCTTAGCTTGTG	2017
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Db	1864	CTGCTCTCCCACTTCCAGCTATCAATTAAGCTCGGCCAAATTCACCCCTTGACTTGGAAAT	1923
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Db	1924	TGACAGGTCAGCTAGAAAGAACATTTGAATCTTCATGTGGTATCCAGAGAAAGAAATTAACA	1983
Oy	2138	GCCCCATTTACAAATTCATCATGATGATATGAAAGTGCATATGACACAGCCAGGGCTGTGGC	2197
Db	1984	GTCCCATTTAACAACTTTGTGATTTGACATGATGAAGATGACATACAGACCCAGGGGTATATGC	2043
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Db	2044	ATTACACAGAGGAAGTTCTCGAATCTCATACAACTGACAGTTGAATTTGTCTCCGATAG	2103
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 AUTHORS Volker, H., Haseel, B., Wolff, J.M., Frank, R. and Rathjen, F.G.
 TITLE Structure of the axonal surface recognition molecule neurofascin
 and its relationship to a neural subgroup of the immunoglobulin
 superfamily
 JOURNAL J. Cell Biol. 118 (1), 149-161 (1992)
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 AUTHORS Volker, H.
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5: /cgn2_6/prodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/prodata/2/ina/backfile1.seq:*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3233.6	78.2	6384	4	US-09-976-594-724 Sequence 724, App
2	2236	54.1	3943	4	US-08-506-2968-27 Sequence 27, App1
3	471.2	11.4	7647	4	US-09-566-921-75 Sequence 75, App1
4	405.8	9.8	3783	4	US-08-506-2968-20 Sequence 20, App1
5	351	8.5	3774	2	US-08-341-8438-1 Sequence 1, App1
6	351	8.5	3774	2	US-08-427-4978-1 Sequence 1, App1
7	351	8.5	3774	2	US-08-427-4978-2 Sequence 2, App1
8	347	8.4	3888	4	US-08-506-2968-13 Sequence 13, App1
9	316.2	7.6	3189	2	US-08-427-4978-3 Sequence 3, App1
10	228.8	5.5	2600	2	US-08-427-4978-4 Sequence 4, App1
11	157.4	3.8	3991	4	US-08-506-2968-3 Sequence 3, App1
12	148.4	3.6	1794	2	US-08-427-4978-5 Sequence 5, App1
13	128.2	3.1	455	4	US-09-621-976-3173 Sequence 3173, App
14	99.8	2.4	1042	2	US-08-427-4978-6 Sequence 6, App1
15	65.2	1.6	7218	1	US-08-332-463-14 Sequence 14, App1
16	49.6	1.2	4584	4	US-09-571-479C-5 Sequence 5, App1
17	49.6	1.2	4584	3	US-08-986-485-1 Sequence 1, App1
18	48	1.2	5506	4	US-09-976-594-530 Sequence 530, App
19	46.2	1.1	1067	1	US-08-264-534-7 Sequence 7, App1
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22	46.2	1.1	1067	3	US-08-893-828-7 Sequence 7, App1
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25	44.6	1.1	6263	4	US-09-023-655-1473 Sequence 1473, Ap
26	41	1.0	832	4	US-09-621-976-2813 Sequence 2813, Ap
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31	40.2	1.0	1014	2	US-08-414-657D-5 Sequence 5, App1
32	40.2	1.0	1014	2	US-09-135-080-7 Sequence 7, App1
33	40.2	1.0	1238	2	US-08-414-657D-3 Sequence 3, App1
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36	39.8	1.0	3360	1	US-08-408-093-5 Sequence 5, App1
37	39.8	1.0	3360	1	US-08-408-420A-5 Sequence 5, App1
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42	39.2	0.9	861	2	US-08-414-657D-9 Sequence 9, App1
43	39.2	0.9	912	2	US-08-414-657D-6 Sequence 6, App1
44	39.2	0.9	927	2	US-08-414-657D-7 Sequence 7, App1
45	39.2	0.9	974	2	US-08-414-657D-1 Sequence 1, App1

ALIGNMENTS

```

RESULT 1
US-09-976-594-724
; Sequence 724, Application US/09976594
; Patent No. 6673549
; GENERAL INFORMATION:
; APPLICANT: Funness, Michael
; APPLICANT: Buchbinder, Jenny
; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
; FILE REFERENCE: PA-0041 US
; CURRENT APPLICATION NUMBER: US/09/976,594
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/240,409
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 1143
; SOFTWARE: PERL Program
; SEQ ID NO 724
; LENGTH: 6384
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6673549 201395.4
US-09-976-594-724

Query Match      78.2%; Score 3233.6; DB 4; Length 6384;
Best Local Similarity 89.4%; Pred. No. 0;
Matches 3722; Conservative 0; Mismatches 9; Indels 433; Gaps 5;

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RESULT 2
US-08-506-296B-27
; Sequence 27, Application US/08506296B
; Patent No. 6313265
; GENERAL INFORMATION:
; APPLICANT: Phillips, Greg
; APPLICANT: Cunningham, Bruce A.
; APPLICANT: Crossin, Kathryn L.
; TITLE OF INVENTION: NEURITE OUTGROWTH-PROMOTING POLYPEPTIDES
; TITLE OF INVENTION: CONTAINING FIBROBLAST TYPE III REPEATS AND METHODS OF USE
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute
; STREET: 10550 No. 6313265th Torrey Pines Road, TPC-8
; CITY: La Jolla
; STATE: California
; COUNTRY: U.S.
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/506,296B
; FILING DATE: 24-JUL-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Pilling, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: TSRI 488.0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 554-2937

QY 2018 CTCCTACTCCAACTCCAGCTCCGTTTACAGATGCCAAATCTCCCTTGAATTAGAAC 2077
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 QY 3758 TGAAGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 3817
 DB 3568 TGAAGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 3627
 QY 3818 AAAAGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 3877
 DB 3628 AAAAGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 3687
 QY 3878 TAGTGAATGAAGAGGCTTATGCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 3937
 DB 3688 TAGTGAATGAAGAGGCTTATGCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 3747
 QY 3938 AATTAAGAGTGAAGAGGAGGCTTATGCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 3997
 DB 3748 AATTAAGAGTGAAGAGGAGGCTTATGCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 3807
 QY 3998 CTCTGTCAAGGCTTATGCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 4051
 DB 3808 CTCTGTCAAGGCTTATGCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 3861

RESULT 3
 US-09-566-921-75
 ; Sequence 75, Application US/09566921
 ; Patent No. 668288
 ; GENERAL INFORMATION:
 ; APPLICANT: Loxing, Jeanne F.
 ; APPLICANT: Tingley, Debora W.
 ; APPLICANT: Edwards, Carla M.

Db 272 ATTCGGCTCTTCACCATCGAAGCAACAGCTTTGCCCCAGAGGTTCCAGGGCATCT 331
Qy 476 ATCAGGTGACAGAAAGAAAGACGGGAGCTGCAGTTTCTAATAATCTGTTGCCGC 535
Db 332 ATCGCTGTATGCGACAAATAGCTAGAACTGCGATGCGATGATCCAGCTGTGG 391
Qy 536 CATCCAGATCACCATGTGAGCAACAAAGAAAATTGAACCAATCACTTCAAGTGTG 595
Db 392 CCGAGGTCGCCCAAGTGGCCGAAGAGACGTGTAACCTGTGGAAGTGGAGAGAG 451
Qy 596 AGCTTTAGTACTTCCCTCGAAGCCCCAATGGAATTCACACCTTAATATTTTGA 655
Db 452 AATCAGTACTGCTGCTTCAACCTCCACCCAGTGCACCCCACTAGATCTACTGA 511
Qy 656 TGGATATTCCTTTCAAGACTTCCACAAAGTAGAGATTTCTCAAGTTTGAANTGGG 715
Db 512 TGAACGCAAGATTTTTCGACATCAACAAAGATGAGGGGTGTCATGGGCCAGAAATGG 571
Qy 716 ACCTTATTTTTCATGTCCTCCAGAGAGACACCGCGAAGACTATATCTGTTATGCTA 775
Db 572 ACTTAATTTTTCGCAATGTCTTACTCAGACAAATATTCAGATCATCTGCAATGCC 631
Qy 776 GATTTAATCATCTCAACCATACAGCAGAAAGCAACCTATTTCTGGAAGTGTATTCAG 835
Db 632 ACTTCCCTGTACCCGAGCATCATTCAAAGAGAACCTATGTAGCTCCGGGTCAAGCCA 691
Qy 836 TGGATGAATTTGAATGACATATAGCTGTAAATTTGAGTACACTGAGTTTATGTCGA 895
Db 692 CCACAGCATGATGAC----- 709
Qy 896 AATCAAGTAGAGAGAGGCCACCAATTTTAACTCCAGAGGCAATGCAATGCAAG 955
Db 710 -----GGAAGCCAGCTCTCTCTTTCCCAAACTCCAGACGCGCTGG 754
Qy 956 AGGAATTAAGAGAAATGTCTTCACTGAGTGCATTGCAAGAGACTGCTCAACCCAA 1015
Db 755 TAGCCTTGACGGCCAGTCAATGATCTGGAGTGCATTGCTGAGGATTCCTCAACCCA 814
Qy 1016 TTATTTACTGGGCAAGAAAGATGGAATGCTAACCCAAAACAGGACGTTTAAAGACT 1075
Db 815 CCATCAAGTGGCTGCCACCCAGTGAACCAATGCAACAGACGTTTATCTCAAAAAC 874
Qy 1076 TTGAGAAAACCTTGACATCATCTGATTTTCAGAAAGCAGACTCTGGAATTAACATGTA 1135
Db 875 ACAACAAGACCTTGCACTACTCAATGTGGGCAAGAGACGATGCGAGTAACTGTGCC 934
Qy 1136 TAGCAAAAATGCAATTAGAGCCATCCACCATACATTTCTGTTAGATTAAGCGGCTC 1195
Db 935 TTGCTGAGAACTGCTGGGCAAGTCCGGCATGCTTAATGTTACTGTGAAGCTGCC 994
Qy 1196 CATCTGGAATCACAGCCCTCAAAAATCTTGTGCTGCCAGAGAGAGATGGGACCTTGA 1255
Db 995 CATATTTGCTGCAAGAGCCCAAGAGCCATTTGTATGTCAGAGAGACTGCCCGCTGAG 1054
Qy 1256 TCTGACAGACTAATGCAACCCCAACCCAGAAATGAGTGTGTTAAACAAATGAGTCCAA 1315
Db 1055 ACTGCAATGTCAGGGCAGGCCCAACAGAGATCACTTGGAGATCAACAGAAATGTCTA 1114
Qy 1316 TAGAAATTTGCCCTGATGACCCCAAGAAAATAGATGCGATACATTAATTTTCA 1375
Db 1115 TGGAGACGGTGAACAGAGACAGAAATGACCGGATGAGAGGGGTCTGATCTTGAGTA 1174
Qy 1376 ATGTTAAGAAAAGATCAAGTGCATATATCAAGTGCATGCTCTTAATGAAATGATATT 1435
Db 1175 AGGTGAGGCAACTGACAAATGATGACCAAGTGAAGCCGCAACGACAGGGCTCC 1234
Qy 1436 TACTGCAACGCAATTTGTAATGTGCTGCTGAGCACACGAAATCTCAACCTGCA 1495
Db 1235 TGTACCAATGCTTCAATTTATGTTGTCCAGCTGCACAGATCTTAACAAAAGACA 1294
Qy 1496 ACACACTTACAGGTCAATTGCAACAGGCTGCTTAACTGACTGCTTCTTTGGGT 1555

Db 1295 ATCAGACATATACATGACATGAGGCACTGACTGTTACTTCTGTGCAAGCCTTTGAG 1354
Qy 1556 CTCTCTCCCAACCATGAGTGTGTTAAAGAGCTTAAAGAAAGTCTCTTCAAGAAATA 1615
Db 1355 CTCTGTTTCCAGATTCAGATGTGCTGATGAAGAAAGAACCAAGTCTTCAAGATGAAC 1414
Qy 1616 TTTATGTTTACATGAATAATGGAATCTTTGAAATCAAAAGATGCTACATGATCGTTAAAG 1675
Db 1415 GATTTTCCCTATGCCAATGGAACGTGACATCAGAGACCTCCAGGCCAATGACACTG 1474
Qy 1676 AATTCCTGTGCCCCAAAAGACAGTACAGAACTTAATAGTGTGTTGCAAGAAATTAAT 1735
Db 1475 GACGTATTTTGTGCAAGCTGCAATGACAGAACTATGTAACATTTTGGCTAAC 1534
Qy 1736 TAGGATGCAAAAGATGAATGATCACTTAACGCCCAATATGCAATGTTGCAAGAGGA 1795
Db 1535 AGGTTAAAGAAACCAAGATCAACAGGGGCCCGGAGGCAATTAAGAAAGATG 1594
Qy 1796 GCATGTTCTTTGATGATGCAAGATGAAACATGATCAACCTTATCCCTCACTGTCTGT 1855
Db 1595 CAAGGTGACATTCAGTGCAGGCTCCTTTGACCTCTTTCAGAGGCCAGATCACTT 1654
Qy 1856 GGC-----TGAAGACAAAGGAACTGCCAGATGAAAGTTCACGTGACA 1906
Db 1655 GGCCTGAGATGAGAGAGACCTACAGAACCTGGGACAGTGAAGATTTTCAATGAAG 1714
Qy 1907 AGGATCATCTAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1966
Db 1715 ATGGAAATCTATGATCCAGAGCTGAGTACAGTACAGAGGCAATCACTGATGTGTGG 1774
Qy 1967 CCACACCACTCTGACAGGCTCTCCGACAGGCTGTGCTTACGTTGTCTCTACTC 2026
Db 1775 CCAGCACTGAATCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1834
Qy 2027 CAATCAGCTCCCTTTAAGATGATGATGATGATGATGATGATGATGATGATGATG 2086
Db 1835 GGCAGTGTCTCACTGGA- GCTGTGCAAGCCGCACTGTGGAACAGAGCA----- 1886
Qy 2087 AACTGACAAAAGTTCAGCTGATGATGATGATGATGATGATGATGATGATGATGATG 2146
Db 1887 -----GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1933
Qy 2147 CAATAATCATCATGATATGAAATGATGATGATGATGATGATGATGATGATGATGATG 2206
Db 1934 AGAAGATGACATTAATTTGAGACAAAGAAATGCTCTGGAATATGATGATGATGATG 1993
Qy 2207 CTGAAGTTTCTGGAACAGACACACCCAGCTGAACCTGTCTCTTAACGTAATCTACT 2266
Db 1994 GCAGGTGCAAGAAATGACATCTTACTTACCTTCAAGCTGTCTCTTATGTCACTCA 2053
Qy 2267 CTTCCGCGTATGCAAGACATGATGATGATGATGATGATGATGATGATGATGATGATG 2326
Db 2054 CTTTTCGGGTCTGCTCAATTAACAAATATGCTCTGAGAAACCCAGCCCTGTCTTGA 2113
Qy 2327 AGTATTTGACGAAGCCTCAGAACAGATTAACCCCAACAGCTGTGAAAGACTGGAT 2386
Db 2114 GTGTGTGACACCTGAGGAGGCCAGAGAAAGAACTGTGATGATGAGGAGAGGGA 2173
Qy 2387 CAGAGCTGATTAATTTGAGATTAAGTGAAGACCTTGAATGTTTCAATTAATGAGG 2446
Db 2174 ATGAGACCAAAATATGTCATCATATGAAGCCCTTTCGTTGATGATGATGATGATG 2233
Qy 2447 CAGGCTTCAGTACAAAGTTAGCTGAGCCAGAAAGATGATGATGATGATGATGATG 2506
Db 2234 CCAAGATTCAGTACCGTGTACAGTGTCTTCCAGAGGCAAGCAGAGACCTGAGAAAC 2293
Qy 2507 TGTGTGTGCAATGATATCAATATATTTGCTCAGGACAGCCCACTTTGTTTCATAC 2566
Db 2294 AGACGGT---AGCACCTTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2350
Qy 2567 TGATCAAAAGTCAAGCCCTGAATGATGATGATGATGATGATGATGATGATGATGATG 2626
Db 2351 AGATCAAAAGTCAAGGAGTGAACCAACAGGGCCAGAGGCTGTGAGCCCAAGTCAACATTTG 2410

QY 2627 GACATCTGAGAGAGACCTCCCAATGATGAGCTCTGGAGACGTCGTGTAATGTGTGA 2686
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 Db 2411 GCTATTACAGGAGAGAGCTACCCCAAGTGAAGCTTGAATGACATCATCTTCA 2470
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 QY 2687 ACAGTACCTTGAAGGAGTGCATCTGGAGCCAGTACCTCTGAAAGCATCCGAGACACC 2746
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 Db 2471 ACTCAAGTACTGTGTCTGTCAGGTGAGAGGCTGTGAGCTTGGCCAGGTTAAAGGCCACC 2530
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 Db 2531 TCAGGAGATACATGTATACATCTGTGAGAGGCGAGCCAGAGAAAGCACAGAGAGAGC 2590
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 QY 2807 ACATTTAGAAAAAATCTCTCACTTCCAAAGGACAGAGACTCTGAGCATGTTCCCGAGCC 2866
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 QY 2867 TAGAGCCCTTTAGACCTACACACTGATGTCCGAGTGTCAATGGGAAAAGGGAGGCC 2926
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 QY 2987 TGAAGATGTGATTCACACACTGAGCTCTCTCACTTTGGAATGGATTCACGAGCCACC 3046
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 Db 2768 TACACTGAGTGTCTGAGTGCAGACCTAGTGTCTGCTACTGCACTGGCCACCACTAGACC 2827
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 Db 2888 A-----GCAGTGTCTTCAACCTTTCGAGCCAGAACTCCGACATCATATCTGA 2938
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 QY 3287 TAGGTGACAGGCAAGTTCAAGCTGTAAATACAGATCAGCAATCTTACTGCTGACGCTG 3346
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 Db 3161 TACCAAGAGGAGAAAGAGGAGCCGATGACCAAGCTCAGCTCAGTATGTAGTACATC 3220
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 Db 3221 AGAGCTCTTACACACATGGAACCTCAGCTGACACAAATATGAGATCCACTATAT 3280
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 Db 3281 AGAGAGAGGCTCTCTGACCATCTGAGATGTGAAGCTAATGAACTGGCCCTGTGCGAG 3340
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 QY 3587 CAGCCGAGAGTGAATATGCAACTCAGGCTGTGTCAATGCTGATGTGTGCTGTTG 3646
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 Db 3341 TTTCTACTACAGGAGCTTTGCTCGAGGGCGTGTTCATCGCTTGTGTAGGCTATCA 3400
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 QY 3647 CTCTCTTATCTTAATTTTGTGATGTTGCTTCAATCAGAGAAACAAAGGTGTGAAT 3706
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 Db 3401 TTCTCTTGTCTCTCATCTGCTCATCTCTGCTTCAATCAAAACGACAGAGGTGTGCAAA 3460
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QY 3707 ATCCAGTTAAAGAAAAAGAGATGCCCATGTGACCTTGAAATCCAGCTTATGAGAGAG 3766
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 Db 3461 ACTCAGTGAAGAGACAGAGAGACCTCAGGTGATTCGAGGCCCGGCCCATGAAAGAGC 3520
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 QY 3767 ATGATGGACATTTTGAAGATACAGTGTGAGAGACCAAGACCTTTGAAAAAGAA 3826
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 Db 3521 AGACCTTCGGCAGATACAGGTCTCTGAGAGTGAACATGAAAGAGAGCCCTTGGCAGA 3580
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 QY 3827 GTGCACTCTCTCAGACAGACTGTGAAAAAAGATATGAGACGACAGCTAGTTAGCT 3886
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 Db 3581 GCCAGCATCTCTCAACGAGAGACATCAACCCCTAGCAGTATGACAGCTGCTGATT 3640
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 Db 3641 ATGGGGGAGGTGTGAGCGTCCAGTTCAATGAGATGCTCTTCAATGAGCCAGTACAGT 3700
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 QY 3947 GTTAAAGAGAAAGAGCCGCTGAAAGAAAGAAAGCTCAAGGCACTTCTCTGTCA 4006
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 Db 3701 GCAGAAAGAGAAAGAGGAGGAGGAGGCAATGACAGTTCAAGGGCTACTCTCTATCA 3760
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RESULT 5

US-08-341-843B-1
 ; Sequence 1, Application US/08341843B
 ; Patent No. 5872225
 ; GENERAL INFORMATION:
 ; APPLICANT: Lemmon, Vance
 ; TITLE OF INVENTION: A Method for Characterizing the
 ; TITLE OF INVENTION: Nucleotide Sequence of L10M and
 ; Patent No. 5872225
 ; TITLE OF INVENTION: the Nucleotide Sequence
 ; TITLE OF INVENTION: Characterized Thereby
 ; NUMBER OF SEQUENCES: 39
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSER: Pay, Sharpe, Beall, Fagan,
 ; STREET: 1100 Superior Avenue
 ; CITY: Cleveland
 ; STATE: Ohio
 ; COUNTRY: U.S.A.
 ; ZIP: 44114-2518
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb
 ; MEDIUM TYPE: storable
 ; OPERATING SYSTEM: DOS 5.0
 ; SOFTWARE: ASCII
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/341,843B
 ; FILING DATE: No. 5872225ember 18, 1994
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 07/904,991
 ; FILING DATE: June 26, 1992
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Minnich, Richard J.
 ; REGISTRATION NUMBER: 24,175
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (216) 861-5582
 ; TELEFAX: (216) 241-1666
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 3774
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear

2024 CTCCTCACTCCAGTCCCGTTTACGATGTCCCAATCTCCCTTTGACTTGAAGTACAG 2083
1835 CTGGGCGCGGT-GCCAGCGCTGCTGTCTGTCCAGCTCCTGTGTGACGAGAC----- 1887
2084 ATCAACTTGAACAAAGTGTTCAGCTGTCAAGACCCGAGCGATGACCAATATGACCCCA 2143
1888 -----CAGGTGCGCGTCTGTGAGTCTGTGAGAGACCAATATGACCCCA 1933
2144 TTACAAATTTCAATCATGCAATATGAAATGCAATGCAAGCCAGGGCTGTGACACACC 2203
1934 TTGAGAAATATGATGATTAATTTGAGAACAAAGAAATGCGCTGAAAAATGTATAGTC 1993
2204 AAATCAAGTTTCTGGAACAGACAGACCCAGCTGAGCTGTCTCTTATGTAATCT 2263
1994 TGGGCAAGTTTCCAGGAAACAGACCTTACACCTTCAAGCTGTGTGCTTATGTCACT 2053
2264 ACTCTTCCGCGTGTAGTGAAGTGAACAGATTTGGAAAGACTTGGCCAGCGAGCTGTG 2323
2054 ACACCTTTAGGGTTACTGCGCATTAACAAATATGCGCCGCGGAGGCCAGCGCGTCTGTG 2113
2324 AGCAGTATTTGACGAAAGCTCAGAACAGATTAATAAATCCACAGCTGTGGAAGACTGG 2383
2114 AACTGTGTGACACCTGAGGAGAGCCGAGAGAAAGACCTGTGATGTGAAGGGGAAAG 2173
2384 GATCAGAGCTGATTAATTTGAGATTAAGTGAAGGCTTGAATGTTTGAATCTAATG 2443
2174 GAAATGAGACACCAATATGTGTATCATCTGTGAAGCGCTCGGTGTGATGTGACTGAAAG 2233
2444 GGCAGAGCTTGTGATCAAAAGTTAGCTGCGCCGAGAAAGATGTGTATGATGATGACAT 2503
2234 CCCCCAGGTTCAATCCGCTGTGACAGTGGCGCTCAGAGGAGACAGAGGCGCTGTGACAG 2293
2504 CTGTGTTTGTGGCAATGTATCCAAATATATTTCTCAGGACAGCCACTTTGTTCAT 2563
2294 AGCAGATTTGT---CAGCGACCCCTTCTGTGTGTGTCACACGTCCACTTGTGTCCT 2350
2564 ACTGTCAAGTTTCAAGGCTGGAATGATGATGATGATGATGATGATGATGATGATGATGAT 2623
2351 ATGATGATCAAGTCCAGGCGCTGTCACAGCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2410
2624 TGGGCACTTCTGAGAGAGACTTCCCAATGTGTGCTCTGTGGAACGTGCTGTGATGATG 2683
2411 TGGGCTACTGTGAGAGAGACTTCCCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2470
2684 TGAACAGTACTTGAAGCGAGTGTGACCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2743
2471 TCAACTCAAGTCCGCTGTGTGTCAGAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2530
2744 ACTTCAAGGCTATGCGATTTTACTATTTGAGAGCCAGAGTTTCAATTAAGAAAGACAG 2803
2531 ACTTCCGCGGATCAATGTGAGTACTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2590
2804 GTTCACTTGAAGAAAGATCTCACTTCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2863
2591 GACATATCAAAAAGACATGT 2650
2864 GGTGAGGCTTTTGAAGCACTACAGTGAATGTCCAGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2923
2651 GCTTGGGCGCTTATAGTCTTACACCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2710
2924 GGCAGGCGAGGCTGACAGAGCTTAAATCTCCAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2983
2711 GGCAGGCGAGG---GAGTTCACCTTTCAGACCCCAAGAGAGAGGAGGAGGAGGAGGAGGAGG 2967
2984 CTTTGAAGATTTGATTCAGACAGTGTCTCTCACTTTGAGATGGAATTCAGCCAGGCG 3043
2768 CGTTGACCTGAGAGTGTGAGTGAACAGAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2827
3044 ACCCGAATGCAATTTTGAAGTGTGACAGTGTGACCTTAAAGTATGAGGCAATTAACAGACAG 3103
2828 GCCACAAAGCGGT 2878

3104 AATTAGGCGCTCTGTGTGATTTGAAATTTCTGCCAACAAGACAGGTGACTTTAAATA 3163
2879 AGGGGGGAGAGGGGAGACGTCTTCAACCTTGTGGGAGCCCGAATTTGGACACACCAAC 2938
3164 AATTAAATTTGACACTGTGATTAAGTTTATTTTATGTACAAACATAGAGGATCAG 3223
2939 TGACGATCTCAGCCCGCCACCTGCGGTACCGCTTCAGCTTACAGGCGACCAACAAAGAG 2998
3224 GAAGTCAATTAACAGAGAGGAGTACAGTGTGATGAGTGTGATTTCTTCCACCTG 3283
2999 GCGCT-----GTTAGGCCATCTTACGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3041
3284 ATGTAGGTGACAGGCAAGGTTCAAGCTGTAAATACAGAGATCAGCAATCTTACTGTGAG 3343
3042 GTCTGGGATCTCAGATTTTGGACATCTCAGCCACAGAGGGGTGAAAATCAAGTGTGT 3101
3344 CTGCTGAGACTATGCCAATATCACTTGTGGAATATGAGGAGGAGGAGGAGGAGGAGGAGG 3403
3102 CTCTGTGGTCCCAAGAGGCGCAGT---GCAACTTCAGGTTCCATATCTTGTCAAAGCC 3159
3404 ATGTTGAATATGTGTAGCAGCAGCAAAAGAAATGAGAAATGTAATGTGT 3463
3160 TTGGAGAGAGAGAGGAGTGGGCTTCTCTTCTG-----CCACAGTATGTCACTTAC 3211
3464 CTGAGAGCTTCTTGTGTTAAAGGCTTATGCTATGCTCAGGAAACAGCATTAAGTTGAGT 3523
3212 ACCAGAGCTCTTACAGCAGGAGTGGGAGCTGAGCTGACACTGATCAGAGATCTCACTGT 3271
3524 GTGCTGTGGGAGCTGTGTTTGTGAGTTTCAAGAGATGTGTTGAGACAGGCGCAGGAG 3583
3272 TTAAAGAGAGAGTGTTCGCGCACCAATGTGTGTAAGACCAATGACAGGCGCGGTGA 3331
3584 TGGCAAGCGGAGGTGATATGCACTCAGGCGTGTGTTCAATGTGTGATGTGTGTG 3643
3332 GG---CTCCCTCTGT 3388
3644 TTGCTCTCTTATCTTAAATTTTGTGATTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3703
3389 TCATCTCTGTGTCTCTGT 3448
3704 AATATCAGTTTAAAGAAAGAGAGATGCCATGTGACCTTGAATTCAGCTTATGAGAG 3763
3449 AATATCAGTGAAGATTAAGAGAGACACCAAGTGTGACTGTGAGGCGGACGATGAAG 3508
3764 AAGATGATGAGCAATTTGAGAAATACAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3823
3509 ATGAGACCTTGTGCGCAGATACAGTCTCTGAGAGTGAACAGAGGAGGAGGAGGAGGAGG 3568
3824 GAAGTGAAGCTCTTCAAGCAGGACTGTGAAGAAAGAAAGATGTGAGCAGCCTAGTGT 3883
3569 GAGGCGAGCAGTCTGTCACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3628
3884 ACTATGAGAGAGGAGGTTAATGTGCGAGTTCAATGAGAGTGTCTCTTATTTGAGCAATGA 3943
3629 AATTATGGGGGAGCGGTGATGT 3688
3944 GTGTGAAGAGAGAGAGAGCGGCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 4003
3689 GTGGCAAGAGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3748
4004 TCAAGCG 4010
3749 TCAACCC 3755

RESULT 6
US-08-427-497B-1
; Sequence 1, Application US/08427497B
; Patent No. 5969124
; GENERAL INFORMATION:
; APPLICANT: Lemmon, Vance
; TITLE OF INVENTION: A Method for Characterizing the
; TITLE OF INVENTION: Nucleotide Sequence of L1CAM and

Patent No. 5969124
TITLE OF INVENTION: the Nucleotide Sequence
TITLE OF INVENTION: Characterized Thereby
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pay, Sharpe, Beall, Fagan,
ADDRESSEE: Minnich & McKee
STREET: 1100 Superior Avenue
STREET: Suite 700
CITY: Cleveland
STATE: Ohio
COUNTRY: U.S.A.
ZIP: 44114-2518
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb
MEDIUM TYPE: Storable
COMPUTER: Compaq Prolinea 5100e
OPERATING SYSTEM: DOS 5.0
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/427,497E
FILING DATE: April 24, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/904,991
FILING DATE: June 26, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Minnich, Richard J.
REGISTRATION NUMBER: 24,175
REFERENCE/DOCKET NUMBER: CWR 2 149-3-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (216) 861-5582
TELEFAX: (216) 241-1666
TELEX: (216) 980162
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3774
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: nucleic acids
HYPOTHETICAL: irrelevant
ANTI-SENSE: no
ORIGINAL SOURCE:
ORGANISM: Homo Sapiens
INDIVIDUAL ISOLATE: 17-18 week fetus
IMMEDIATE SOURCE:
LIBRARY: Stratagene cDNA Library 936206
CLONE: synthesis of 4 clones
PUBLICATION INFORMATION:
AUTHORS: Hlavin, Mary Louise
AUTHORS: Lemmon, Vance
TITLE: Molecular structure and functional
TITLE: testing of human L1CAM: an
JOURNAL: GENOMICS
VOLUME: 11
ISSUE:
PAGES: 416-423
DATE: 1991
RELEVANT RESIDUES IN SEQ ID NO: 1 to 3774
US-08-427-497E-1

Query Match 8 5%; Score 351; DB 2; Length 3774;
Best Local Similarity 46.2%; Pred. No. 2.2e-93;
Matches 1749; Conservative 0; Mismatches 1900; Indels 138; Gaps 12;

QY 239 TGGTACAGCTCCACCATCACCAAGTCTCCAAAGATTACATTATTGACCTCGGG 298
DB 92 TGTATGAGCCACCTGTCATACCGAAGAGTCTCCAGCGCGCTGTGTTCTTCCACAG 151
QY 299 AGAATATTGTAATCCAGTGTGAAGCCAAAGGAAACCGCCCAAGCTTTTCTGAGCC 358

DB 152 ATGACATCAGCTCAAGTGTGAGGCCAGTGGCAAGCCGAAAGTGCAGTTCCGCTGAGCA 211
QY 359 GTAATGGAGCTCATTTTGAATGATGATTAAGACCTCTGTGTCACATGAA-----GCCTG 412
DB 212 GGGATGGTGTCCATTTCAACCAAGAGAGAGCTGGGTGTGACCGGTGATCCAGTGGCCCC 271
QY 413 GCACAGAAACGCTCAATTAATTAATCATGAGCGAAAGGAAAGTGAACCTATGAAAGAG 472
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QY 473 TCTATCAGTGTACAGCAAGAAACGAGAGCTGCAAGTTCTATATAATGTTGTCC 532
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3404 ATGTAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3463
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Db 3749 TCACCC 3755

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RESULT 7

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US-08-427-497E-2
; Sequence 2, Application US/08427497E
; Patent No. 5969124
; GENERAL INFORMATION:
; APPLICANT: Lemmon, Vance
; TITLE OF INVENTION: A Method for Characterizing the
; TITLE OF INVENTION: Nucleotide Sequence of L1CAM and
; Patent No. 5969124
; TITLE OF INVENTION: the Nucleotide Sequence
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fay, Sharpe, Beall, Fagan,
; STREET: 1100 Superior Avenue
; CITY: Cleveland
; STATE: Ohio
; COUNTRY: U.S.A.
; ZIP: 44114-2518
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb
; MEDIUM TYPE: Storable
; COMPUTER: Compad Prolinea 5100e
; OPERATING SYSTEM: DOS 5.0
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/427,497E
; FILING DATE: April 24, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/904,991
; FILING DATE: June 26, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Minnich, Richard J.
; REGISTRATION NUMBER: 24,175
; REFERENCE/DOCKET NUMBER: CWR 2 149-3-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (216) 861-5582
; TELEFAX: (216) 241-1666

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; TELEX: (216) 980162
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3774
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: nucleic acids
; HYPOTHEICAL: irrelevant
; ANTI-SENSE: no
; ORIGINAL SOURCE:
; ORGANISM: Homo Sapiens
; INDIVIDUAL ISOLATE: 17-18 week fetus
; IMMEDIATE SOURCE:
; LIBRARY: Stratagene cDNA Library 936206
; CLONE: synthesis of 4 clones
; PUBLICATION INFORMATION:
; AUTHORS: Hlaavin, Mary Louise
; TITLE: Molecular structure and functional testing of
; TITLE: human L1CAM: an interspecies comparison.
; JOURNAL: GENOMICS
; VOLUME: 11
; ISSUE:
; PAGES: 416-423
; DATE: 1991
; RELEVANT RESIDUES IN SEQ ID NO: 1 to 3774
US-08-427-497E-2

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Query Match 8.5%; Score 351; DB 2; Length 3774;
Best Local Similarity 46.2%; Pred. No. 2.2e-93;
Matches 1749; Conservative 0; Mismatches 1900; Indels 138; Gaps 12;

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2879 AGGGGGGCAAGGGGCAACTGTCTTCAACCTTGGGAGCCCGCACTTCGAGACACAAAC 2938
3164 ATTTAATTTACAGACTCCATATTAATTTATTTATTCATGACAAATATACAGAGATCAG 3223
2939 TGAACCATCTACGCGCCACCTGCGATCCGCTTCCAGCTTCAAGGACACCAACAAAGAG 2998
3224 GAAGTCAATTAAGAGAAAGAGAGTCAACATGTGTGATGAAGTGTATTTCTTCCACTG 3283
2999 GCCCT-----GTAAGCCATCTGATCGGAAAGAGGACATATGCGCTT 3041
3284 ATGTAGTGCAGGCAAGTTCAAGCTGTAAATACAGATCAGCAATCTTACTGCTGACG 3343
3042 GTCTGGATCTCAGATTTTGGCAACATCTCAGCCACAGGGGGTGAAGAACTACAGTGTCT 3101
3344 CTGCTGAGACTATGCCAATATATGTTGGAAATATAGGAGACCAAGCATGGAATTTT 3403
3102 CTCTGGGTCCCGCAGAGGCGCAGT--GCACCTTCAAGTTCATATCTTGTCAAAAGCC 3159
3404 ATGTGAATATGTGTATAGCAGCAGCAAGAAAGAAATGTAATGTT 3463
3160 TTGGAGAAAGAGAGGTGGGGCTTCCCTTTC-----CCACATATGTCAGCTTAC 3211
3464 CTCGAGCTCTTCTTGGGTTTAAAGGCTTATGTCAGAGAAACAGCATCAAAAGTTGAGTTG 3523
3212 ACCAGAGCTCTTACAGCAGATGGGACCTGACGCTGACATGACTAGATCACTTGTG 3271
3524 GTGCTGTGGGGAATCTGTTTGTGATTCAGAGATGTGTTGAGACAGGCGCCAGCA 3583
3272 TTAAAGAGAGAGATGTTCCGACCAATGCTGTGAAGCAATGAGCAGGCGCGGTGA 3331
3584 TGGCAAGCGGCGAGTGAATTTGCAACTCAGGGCTGTTTCAATGTCATGATGTGCTG 3643
3332 GG---CTCCCTCTGCTGCTGCTTGCACATGAGGCTGTGTTTCACTGCTTGTGATGCCA 3388
3644 TTGCTCTCTTATCTTAATTTTGTGATTTGTTGCTTCAATCAGAAACAAAGGTGTTA 3703
3389 TCACTCTCTGCTCTGCTGCTGCTCATCTCTGCTTCAATCAAGCCAGCAAGGCGGCA 3448
3704 AATATCAATTTAAAGAAAGAAAGATGCCATCTGACCTGTAATTCAGCTTATGAAG 3763
3449 AATATCAATTTAAAGAAAGAAAGATGCCATCTGACCTGTAATTCAGCTTATGAAG 3508
3764 AAGATATGAGCAATTTGAGATATACATGATCAGAGCAACAGCCTTTGAAAAAG 3823
3509 ATGAGACCTTGGCGAGTACAGTCTCTGAGATGACAGAGAAAGGCGCTTTGGCA 3568
3824 GAAGTCAACTCTTCAAGCAGACTGTGAAAAAAGAAATAGTGAACAGCCTTATGTTG 3883
3569 GCAGCAGCATGCTCAACGAGGACATCAAGCCCTGGGCAATGACAGCCTGCGCG 3628
3884 ACTATGAGAGAGGCTTATGCGCAATGATGAGATGAGTGTCTTATTTGCAATATCA 3943
3629 AATATGAGGAGCAGCTGATGTTCACTTCAACAGAGATGTTGTTTCAATGAGCAGTATCA 3688
3944 GTGCTAAGAAAGAAAGAGAGCGGCTGAGAGAAAGAAAGCTCAGAGGCACTTCTCTG 4003
3689 GTGCAAGAAAGAGAGAGAGCGGCGCAATGACATCAAGGCGCACTTCCGCCCA 3748
4004 TCAAGC 4010
3749 TCAAGC 3755

RESULT 8
US-08-506-296B-13

/ Sequence 13, Application US/08506296B
/ Patent No. 6313265
/ GENERAL INFORMATION:
/ APPLICANT: Phillips, Greg
/ APPLICANT: Cunningham, Bruce A.
/ APPLICANT: Crossin, Kathryn L.
/ TITLE OF INVENTION: NEURITE OUTGROWTH-PROMOTING POLYPEPTIDES
/ TITLE OF INVENTION: CONTAINING FIBRONECTIN TYPE III REPEATS AND METHODS OF USE
/ NUMBER OF SEQUENCES: 77
/ CORRESPONDENCE ADDRESS:
/ ADDRESS: The Scripps Research Institute
/ STREET: 10550 No. 6313265th Torrey Pines Road, TPC-8
/ CITY: La Jolla
/ STATE: California
/ COUNTRY: U.S.
/ ZIP: 92037
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/506,296B
/ FILING DATE: 24-JUL-1995
/ CLASSIFICATION: 514
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Fitting, Thomas
/ REGISTRATION NUMBER: 34,163
/ REFERENCE/DOCKET NUMBER: TSRI 488.0
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (619) 554-2937
/ TELEFAX: (619) 554-6312
/ INFORMATION FOR SEQ ID NO: 13:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 3888 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: double
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA
/ HYPOTHETICAL: NO
/ ANTI-SENSE: NO
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 12..3773
/ US-08-506-296B-13

Query Match 8.4%; Score 347; DB 4; Length 3888;
Best Local Similarity 46.5%; Pred. No. 3.5e-92;
Matches 1762; Conservative 0; Mismatches 1875; Indels 150; Gaps 14;

239 TGTACAGGCTCCACATCAACCAAGTCTCCAAAGATTACATTAATTCAGCCTCGGG 298
103 TATGAGGCACTCTGTCATACGGAACATCTCCACGCGCTGTGTTGCTTCCACAG 162
299 AGAATATGTAATTCAGTGTGAAGCCAAAGGAAACGCCCCCAAGCTTTCTGAGACC 358
163 ATGACATCAGCTCAAGTGTGAGGCCAGTGGCAAGCCGAAGTGAAGTCCCTGAGCA 222
359 GTAATGGAAGTCAATTTGATCATGATTAAGAACCTCTGTGATCACTGAA-----GCCTG 412
223 GGAATGTGTCACTTCAACCCAAAGAAAGTGGTGTGACCGTGTACAGTGTGCCCC 282
413 GCACAGAAAGCGCTCAATTAATTAATCATCATGAGGGAAGGAAAGCTGAGACTTGAAGAG 472
283 ACTTGGCTCTTCAACATCAAGGCAACAGCACTTGTCTAGAGTTCACAGGGCA 342
473 TCTATAGTGTACAGCAAGAAAGAAAGCGGAGCTGCAAGTTTCTAATAATTTGTTGCC 532
343 TCTACCGCTGCTTGGCAGCAATTAAGCTGGGCAAGCCATGTCATGAGATCCGGCTCA 402
533 GCCCATCAAGATCACTATTTGTGACCAAGAAAGAAAGCTTGAACCATCACTTCAAGT 592
403 TGGCGAGGCTGCCCAAGTGGCCAAAGAGACAGTGAAGCCGTGTGAGGTGAGAGAG 462

AUTHORS: Hlavín, Mary Louise
AUTHORS: Lemmon, Vance
TITLE: Molecular structure and functional testing of
TITLE: human LIGAM: an interspecies comparison.
FUND: none

Query Match	7.6%	Score 316.2	DB 2	Length 3189
Best Local Similarity	46.7%	Pred. No. 4.3e-83		
Matches 1411; Conservative	0	Mismatches 1533	Indels 75	Gaps 10

OY	982	TTGGAGTGCATTGGCAAGAGACGTGCTACCCCAATTAATTCTGGGGCAAGAGMATGGA	1044
Db	237	CTGGAGTGCATGGCGAGGGGCTTTCCACGCCCAACATCAATATGGCTGGCCCCAGTGGC	296
OY	1042	ATGCTACCCAAAACAGACAGCTTTATATAAGAACTTTGAAAACTTGACATCAATTCAT	1101
Db	297	CCCAATGCCAGCTGACCGGTGTCACCTACAGAAACCAACACAGACCTTGAGCTGTGAAA	356
OY	1102	GTTTCAGAAGCAGACTCTGSAATTAACCAATGTATAGCAAAAAATGCAATTGAGACCATC	1163
Db	357	GTGGCGGAGAGAGATGATGGCGAGTACCGGTCTGCTGGCCGAGAACCTCACTGGGCAATGCC	416
OY	1162	CACCATACCAATTTCTGTTAGATTAAACGGCTGCATACCTGGATCAGACCCCTCAAAAT	1221
Db	417	CGGCACTGGTACTATGTACCGGTGAGGCTGCCGCTACTGGCTCACAAGGCCCAAGAC	476
OY	1222	CTTGTCGTCTCCCGAGAGAGATGGGACCTTGATCTGCAAGCTAAATGGCAACCCCAA	1281
Db	477	CATCATATATGGCCGAGAGAGACTGCCCGCTCGACTCCCAAGTCACAGGCAAGGCCCAA	536
OY	1282	CCCAAAATTAAGCTGGTTAAACAAATGAGAGTCCCAATAGAAATTTGCCCTGATGATGCCAGC	1341
Db	537	CCAGAGTCACTCTGGAGAAATCAACGGGATCCTGTGGAGAGAGCTGGCCAAAGCCAGAG	596
OY	1342	AGAAAAATAGATGGCGATACCATTAATTTTTCAAAATGTTCAAGAAAGATCAAGTGCACTA	1401
Db	597	TACCGATTACAGCGTGGCGCCCTGATCTGAGCAACGTGACGCCAGTGAACACAAATGGTG	656
OY	1402	TATCATGTCATGCTCTTAATGAATATGGAATATTTATCTGGCAACGCATTTGTAAATGTG	1461
Db	657	ACCCATATGTAGGCCCCGACACCGGACGAGGCTCTTGCTGGCCAAATGCTTACATCTACGTT	716
OY	1462	CTGGCTGAGCACCAACGAATCCTCAACCTGTCAAAACAACCTTACACAGTCAATTTGCAAC	1521
Db	717	GTCCAGCTGCCAGCCCAAGATCTCTGACTGGGACAAATACAGCTACATATGGCTGTCCAGAGC	776
OY	1522	AGGCTGCTTACTAGACTGTGCTCTTTTGGGTCTCCTCTCCCAACATGAGTGTGTT	1581
Db	777	AGCACTGCTCTACTTCTGTGCAAGGCTTTCGAGGCGCTGTGGCCCAAGTGTTCAGTGGCTG	836
OY	1582	AAAGAGCTAAAGAGAGTGTCTTCAATGAATATTTATGTTTACATGAAGAAATGSACT	1641
Db	837	GACGAGATGGGACACACAGTGTCTTGAGACGAAACGCTTCTTCCCTAATGCCAATGGGACC	896
OY	1642	TTGGAAATCAAGATGTACATGATGCTTAAAGAAATTCCTGTGGGCCCAAAAGGACAGT	1701
Db	897	CTGGGCATTCGAGACCTCCAGGCCAATGACACCGGACGCTACTTGTGCTGGCTGCCAAT	956
OY	1702	ACAGGAATTTATGCTGTGTGTCAGAGAAATTAATTTAGGATGGCAAGATGAAGTTAC	1761
Db	957	GACCAAAACAATGTTACCATATGCTTAACCTGAAGGTTAAAGATGCAACTCAATCTACT	1016
OY	1762	TTACAGCCCGCAATATGACTGTGTGCAAGAGGAGACAGTGTGCTCTTTGAATGCAAAATG	1821
Db	1017	CAGGGGCCCCGACGACAAATGAGAAAGAAAGTTTCCAGGTTGACCTTACAGTGCAGGCC	1078
OY	1822	AAACATGATCAACCTTATCCCTCACTGTCTCTGTGGCTGAAG-----GACACACGG	1872

D	b		1077	TCTTTGACCCCTCTTTCAGACCAGATCACTGGCGTGGGAAGCGTCAGACTCCTCAG	1136
O	y		1873	GAACTGCCAAGTGTAAGAAGTTCACTGTGTGACAAGATCATCTAGTGTAGTGTGC	1932
D	b		1137	GAGCTTGGGGACAGTGAACAAATCTTCAATAGAGATGGGCGCTGTATCACAGCCTG	1196
O	y		1933	AGTAGCATGTACAGGGGACTTACAGCTGTGTGGCCAACACACTCTTGACAGGCTCCC	1992
D	b		1197	GACTACAGCCGACAGGGGCMATTACAGCTGCCTGGCCAGTACCGAACCTGGAATGTGTGGAG	1256
O	y		1993	GCGACGCTGTGCTTAGGTTGGTGTCTCTTACTCCACTCCAGCTCCCGTTTACATGTCTC	2052
D	b		1257	AGTAGGGCAACGCTCTTGTGTGTGGGAGCCCT- GGGCGGCTGCACGGCTGTGTGTCTC	1315
O	y		2053	CCAAATCTCCCTTGTGACTTAGAACTGACAGATCAATTGACMAAAGTGTTCAGCTGTCA	2112
D	b		1316	CGACTGTGACTGTGTGACGAGAGCC-----AGTGCGGGTGTCC	1355
O	y		2113	TGACCCCCGAGCGATGACACATAAGCCCCATTACAAAATTCAATCGAATTAGAAAT	2172
D	b		1356	TGGATCTCTGAGAGAACCAAAATGCCCTTATAGAAATATGACATTGAAATTTGAAGAC	1415
O	y		2173	GCAATGACACAGCCAGGGCTGTGGCACCAACAACTGAAGTTCTGGAAACACAGACCA	2232
D	b		1416	AAGGAATGCGCCTGAAAAATGTATCAGTTGGGCAAGGTTCCAGGGAACCAAGCTCTT	1475
O	y		2233	GCCGAGCTGAAAGCTGTCTCTTTCATGTAACCTACTCTTCGCGCTGATGGCAGTGAACAGC	2292
D	b		1476	ACCAACCTCAAGCTGTGCGCTTATGTCACTACACTTTTAGGGTTATCTGGCATTAACAA	1535
O	y		2293	ATTGGGAAGACTTGGCCAGCGAGGCGCTCTGAGCAGTATTTGACGAAAGCTTCAGAACCA	2352
D	b		1536	TATGGCCCGGGAGGCCAGCCCGCTCTGAGACTGTGTGTCACACTGAGCGAGCCCA	1595
O	y		2353	GATAAAAACCCACAGCTGTGGAAAGACCTGGGATCAAGCCTGATATTTGGAAATACG	2412
D	b		1596	GAGAGAAACCTGTGGAATGTGAAGGGGAGAGAAATAGACACACCAATATGTGTATCAGC	1655
O	y		2413	TGGAAGCCCTTGAATGTGTTTGAATCTAATGTGGCCAGGCTTCAGTCAAAAGTTAGCTGG	2472
D	b		1656	TGGAAGCGCTCCGCTGTGATGTGACTGGAAAGCCCCAGATTCACTACCGCTGTCACTGG	1715
O	y		2473	CGCAGAAAGATGTGTATGTATGTGAATGACATCTGTGTGTGTGGCAATGTATCCAAATAT	2532
D	b		1716	CGCCCTCAGGGGACACAGAGGGCCCTGACAGGAGCAGATGT-- CAGCGACCCCTTCTCG	1772
O	y		2533	ATTGTCTCAGGACAGCCAACTTTGTTCATCTGATCAAAGTTCAAGCCCTTGAATGAC	2592
D	b		1773	GTGTGTGTCAACAGCTGCACCTTGTGTCCTTATGTAGATCAAAATGTCAGGCGCTCAACAGC	1832
O	y		2593	ATGGGGTTTTGGCCCCGACAGCTGTATGTATGTGGGACATTTCTGGAGAAAGCTTCCCAATG	2652
D	b		1833	CAGGGCAAGGACCAAGAGCCCCAGGTCACTATGTGGTACTCTGTGAGAGGACTACCCCAAG	1892
O	y		2653	GTGGCTCTTGGGAAGTGCCTGTGATGTGTGTGAACGTAACCTTAGCCGAGGTGCACCTGG	2712
D	b		1893	GCAATCCCTGAGCTGTGAAGGATTAATCCTCAACTCAAGTGCCTGTGTGTCAAGTGG	1952
O	y		2713	GACCCAGTACTCTGAAAAGCATCCGAGACACTTACAAGGCTATCGGATTTACTATTGG	2772
D	b		1953	CGGCGGTGTGACCTGTGGCCAGGTGTAAAGGGCCACTTCGCGGGAATACATATGACGTATCGG	2012
O	y		2773	AAGACCCAGAGTTTATCTAAAAAGAAACAGAGTCACTTAGAGAAAAAGATCTCACCTTC	2832
D	b		2013	AGGGAGGGCAGTCAAGAGAAAGCACAGBAAGACATATCCAAAGAACCATGTGTGTGTG	2072
O	y		2833	CAGGCGACAGACTTCAATGACATGTGTGCGGGCTTAGAGCCCTTTAGCCCACTACACTG	2892
D	b		2073	CCGCGCAACACACAGTGTCAATCTCAGTGTGTGGCGGCTTATATAGCTCTTACCACTG	2132
O	y		2893	AATGTCCGATGTGTCAATGGAAAAAGGGAGGGCCAGCCCTTACAGAGTCTTAAAT	2952

Db 2133 GAGGTGACGAGCCCTTTAAACGGGCGAGATCGGGGCCCGCCAGC---GAGTTCACTTTCAGC 2189
Qy 2953 ACTCCAGAAAGAGTCCCAAGTCTCCCTGCTCTTTGAAGTTGTGAATCCAACTGAGC 3012
Db 2190 ACCCCAGAGGAGATGCTGGCCACCCCGAGGCGCTTCACTGAGTGCAGTGAACACC 2249
Qy 3013 TCTCTCACTTTGGATGGATTCACCGAGCCAGCCAGATGGCATTTTGAACAGATACACC 3072
Db 2250 AGCTCTGCTGCTGGCGAGCCGCCACTCAGCACAAGGCGTGTCTACCCGGCTACGTCG 2309
Qy 3073 TTTAAGTATCAGCAATTAACAGCACAATGATTAAGCCCTTGTGTAGATTGAAAT 3132
Db 2310 CTCTCTTACCACTCCCTGTGATGAGGGGGGCAAGGGCAATGTCTTCAACTTCGGGAC 2369
Qy 3133 CCGCAACAAGACAGGTGAGCTTTAAATAATTTTGAAGTCTGATTAAGTT 3192
Db 2370 CCGCAACTTGGACAC---ACAACTGACGATCTAGCCCCCACTGGGGTACCCCTTC 2426
Qy 3193 TATTTCTATGCAAAATCAGCAGAGATCAGAAATCAATTAACAGAGAGCAGTACA 3252
Db 2427 CAGCTTCAAGGCCACCAACAAAGAGGCGCTGTGAAGCATGTACGGGAAGGAGCAGT 2486
Qy 3253 ACTGTGATGAGAGCTGTATTTTCACTGATGTAGTGTGAGCAGCAAGTTCAAGCTGTA 3312
Db 2487 ATGG-----CCTTGTCTGGGATCTCAGATTTTGGCAACATCT 2523
Qy 3313 AATACAGAGATCAGCAATCTTACTGCTGACGTGTGAGACTATGCACTATGCAATGAGTGG 3372
Db 2524 CAGCCACAGGGGTAAACTTACAGTGTCTCTCTGGGTCCCAAGAGAGGCCAAT--G 2581
Qy 3373 GAATATGAGGACACAGCATGTGAATTTTATGTTGAATATGATGTAGCAGCAGCAAA 3432
Db 2582 CAATTCAGGTTCAATATCTTGTTCAAAGCCTTGGAGAAAGAAAGAGGTGGGCTTCCT 2641
Qy 3433 GAAAGATGAGAAAGAAATTTGAATGTTCTTCGAGCTCTTGGGTAAAGGTCTTA 3492
Db 2642 TTGG-----CCACAGTATGTCTACCTACMACCAGAGCTCCCTACACGAGTGGACCTG 2693
Qy 3493 ATGCCAGGAACAGCATACAAAGTTGAGTTGAGTGTGCTGGGGGAGCTGTGGTTTGTGAGT 3552
Db 2694 CAGCTTGAACCTGACTGACGATGATCAGTCTTTTAAAGAGAGATGTTCCGGACCAAA 2753
Qy 3553 TCAGAGATGTGTTTGAAGCAGGCCAGCAGTGGCAAGCCGAGAGTGAATATGCAACT 3612
Db 2754 GCTGTAAAGCAATGGCAGGCGCGGTGAGG---CTCCCTCTGCTGTGCTTCGCACT 2810
Qy 3613 CAGGCTGTGTTGATGTGTGATGTGTGCTGCTCTTATTTTAAATTTTGTGAT 3672
Db 2811 GAGGGCTGTGTTCACTGCTTGTGAGTGCATCTCTCTGCTCTGCTGCTCATC 2870
Qy 3673 GTTGTCTATCAGAAAGAAACAGGGGTGTAATATCAGTTAAAGAAAGAAAGATGCC 3732
Db 2871 CTCTGCTTCAACGCCAGCAGAGGGGGGCAAAATCTCAATGAAGTAAGAGAGACACC 2930
Qy 3733 CATGCTGACCCCTGAATTCAGCTATGAGAAAGATGATGGGCAATTTGGAGATACAT 3792
Db 2931 CAGGTGAGCTCTGAGGCGCGACCGATGAAGATGAGACCTTCGCGAGTACAGTCCCTG 2990
Qy 3793 GATGCAAGAGACCAAGCCCTTTGAAAAAGAAAGTGAATCTCTTCAACAGAGACTGTG 3852
Db 2991 GAGAGTGAACAACAGGAGGAGGCTTTGGACGACGACCATCTCAACGGGGAATC 3050
Qy 3853 AAAAAAGAAATGATGACGACGCTAGTGTGATGAGAGAGGGGTAAATGCGCACTTC 3912
Db 3051 AAGCCCTGGGCGAGTACGACGCTGGCGGATTAAGGGGCGAGCGTGTTCAGTTTC 3110
Qy 3913 AATGAGATGGCTCTTATTTGACATACAGTGTGAAGAAAGAAAGAGCCGGCTGAA 3972
Db 3111 AACGAGATGTTCTTCTTATGCGCACTACAGTGTGCAAGAGAGAGAGGGGCGACAGG 3170
Qy 3973 GGAACGAAGCTCAGAGG 3991
Db 3171 GGCAATGACAGCTCAGGGG 3189

RESULT 10
US-08-427-497E-4
Sequence 4, Application US/08427497E
Patent No. 5969124
GENERAL INFORMATION:
APPLICANT: Lemmon, Vance
TITLE OF INVENTION: A Method for Characterizing the
TITLE OF INVENTION: Nucleotide Sequence of L1CAM and
Patent No. 5969124
TITLE OF INVENTION: the Nucleotide Sequence
TITLE OF INVENTION: Characterized thereby
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Fay, Sharpe, Beall, Fagan,
ADDRESSEE: Minnich & McKee
STREET: 1100 Superior Avenue
CITY: Cleveland
STATE: Ohio
COUNTRY: U.S.A.
ZIP: 44114-2518
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb
MEDIUM TYPE: Storable
COMPUTER: Compaq Prolinea 5100e
OPERATING SYSTEM: DOS 5.0
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/427,497E
FILING DATE: April 24, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/904,991
FILING DATE: June 26, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Minnich, Richard J.
REGISTRATION NUMBER: 24,175
REFERENCE/DOCKET NUMBER: CWR 2 149-3-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (216) 861-5582
TELEFAX: (216) 241-1666
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 2600
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: nucleic acids
HYPOTHETICAL: irrelevant
ANTI-SENSE: no
ORIGINAL SOURCE:
ORGANISM: homo sapiens
INDIVIDUAL ISOLATE: 17-18 week fetus
IMMEDIATE SOURCE:
LIBRARY: Stratagene cDNA Library 936206
CLONE: 4
PUBLICATION INFORMATION:
AUTHORS: Hlavin, Mary Louise
AUTHORS: Lemmon, Vance
TITLE: Molecular structure and functional testing of
TITLE: human L1CAM: an interspecies comparison.
JOURNAL: GENOMICS
VOLUME: 11
ISSUE:
PAGES: 416-423
DATE: 1991
RELEVANT RESIDUES IN SEQ ID NO: 1108 to 3708
US-08-427-497E-4
Query Match 5.5%; Score 228.8; DB 2; Length 2600;

Best Local Similarity 45.9%; Pred. No. 3,4e-57;
Matches 1224; Conservative 0; Mismatches 1367; Indels 75; Gaps 10;

QY 1306 GGAAGTCCCAATGAAATTTGGCCCTGATGACCCCAAGAGAAATTAATGATGCGATACATT 1365
 Db 1 GGAATCCCTGTGAGAGAGCTGGCCAAAGACCAAGATACCGGATTCAGGGTGGCCCTGG 60
 QY 1366 ATTTTTCAAATGTTTGAAGAAGATCAAGTGCATATATCATGCAATGCTCTATATGAA 1425
 Db 61 ATCTGAGCAAGCTGAGCCCAAGCTGACCAATATGATACCAATATGATAGCCCGCAACCG 120
 QY 1426 TATGATATTTACTGGCAAAACGATTTGTAATGTGCTGAGCCCAACGATCTTC 1485
 Db 121 CAGGGCTCTGCTGGCCCAATGCTCATCTACATGTTGTCAGCTGCACGCAAGATCTGG 180
 QY 1486 AACCTGCAAAACACTCTACAGCTCATTTGCAAAAGCCGCTCTTATACAGCTGGC 1545
 Db 181 ACTGCGGACATCAAGCATGATGCTGTCAGGAGGACATGCTTACCTTCTGTCAAG 240
 QY 1546 TTCTTGGGCTCTCTCCCAACCATGAGTGTATTAAGAGCTAAAGAGTGTCTT 1605
 Db 241 GCTTTCGAGCCCTGTGCTCCAGTGTTCAGTGTGCTGAGAGATGGACACAGTGTCTT 300
 QY 1606 CATGAAGATATTTATGTTTACATGAAATGAACTTTGGAATCAAGATGCTACATG 1665
 Db 301 CAGGAGAAAGCTTCTTCCCTATGCAATGGGACCTGGGCAATTGAGACCTCCAGGCC 360
 QY 1666 ATCTGTTAAAGAAATTCCTGTGGCCCAAAAGACATGACAGAACTTATACGTGTGCA 1725
 Db 361 AATGACACCGGACGCTACTTCTGCTGGCTGCCAATGACCAAAACATGTTTACATCATG 420
 QY 1726 AGGAATAAATTTAGGATGGAAGAAAGATGATCACTTACAGCCGGAATATGCAATGG 1785
 Db 421 GCTAACCTGAAGTTTAAAGTGCATCTCAGATCATCAGGGGCCCCGACACATGCA 480
 QY 1786 CAAAGAGGAGCATGTGTCTTGTGATGCAAAAGTGAATCATGATCACTTATCCCTC 1845
 Db 481 AAGAAAGTTTCAAGGGTGAACCTTACGTGCAAGCCCTCTTGAACCCCTCTTGCAGCCC 540
 QY 1846 ACTGTCTGTGGTGAAGCAACAGGAACTGCCCCAGTA-----TGAAGGTTTC 1896
 Db 541 AACATCACCCTGGGTGGGACGGTCCAGACCTCCAGAGCTTGGGAGCAGTGCATGATAC 600
 QY 1897 ACTGTGACAGAGATCATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1956
 Db 601 TTCAATGAGAGATGGGGCTGTGATCAACAGCTGGACTACAGCAACAGGCAACTAC 660
 QY 1957 AGGTGTGGCCCAACCACTGTCAGAGCTCTCCGCAAGCGCTGTGCTTATAGCTTGT 2016
 Db 661 AGCTGTGGCCCAATCCGATCTGATGTGTGAGAGATGAGGCAAGCTCTTGTGTGT 720
 QY 2017 GCTCTACTGCAATCTCAGCTCCGTTTACATGATGTCCTCAATCTCTCTTGAATTAA 2076
 Db 721 GGGAGCCCT--GGGCCGGTCCACAGCTGTGTCTGCACTGCACTCTGTCGCGAGAG 779
 QY 2077 CTGACGATCACTTGAACAAAGTGTTCAGCTGTCAATGACCCCAAGCGATGACATCAT 2136
 Db 780 C-----CAGTGGCGGTCTCTGAGTCTCTCAAGACCAACAT 819
 QY 2137 AGCCCATTTACAAATTTCACTCATGATGATGAAATGATGATGATGATGATGATGATG 2196
 Db 820 GCCCATTTGAGAAATATGACATTTGATTTGAGAGCAAGAAATGAGCCCTGAAATATG 879
 QY 2197 CACCAACAACTGAAGTTTCTGAGACACAGACCAAGCCCAAGTGAAGTGTCTCTTAC 2256
 Db 880 TACAGCTGGGCAAGGTTCCAGGGAACAGACCTTACCACTCAAGCTGTGCGCTAT 939
 QY 2257 GTGAATATCTCTTCCGCTGTGATGAGAGTGAACAGATTTGGAAGGCTTTGCCACGAG 2316
 Db 940 GTCACTTACACTTTAAGGTGTACTGCTCAATTAACAAATATGAGCCCGGAGGCCACCG 999
 QY 2317 GGTCTGACAGATTTTGAAGGAGCTCAGAAACGATTAACCCCAAGCTGTGGA 2376
 Db 1000 GTCTCTGACAGCTGTGTCACACCTGAGGAGGCCCAAGAGAACCTGTGATGAG 1059
 QY 2377 GGAAGTGGATGAGAGCTGATATATTTGAGATTTAGTGGAGCCCTGAAATGTTTGA 2436
 Db 1060 GGGAAAGAAATGAGACCAACCAATATGATCATCAGTGAACCGCTCGGTGATGAG 1119
 QY 2437 TCTAAATGGGCGCAGGCTTCAATGAAAGTTAGCTGGCCGCAAGAAATGATGATGAA 2496
 Db 1120 TGAAGGCCCCCAGGTTCAATGACCGGCTGAGTGGCCGCTCAGGGGACACAGAGGCC 1179
 QY 2497 TGAATCTGTGTGTGTGCAAAATGATATATTTGTCTCAGAGCAGCCCACTTT 2556
 Db 1180 TGGCAGAGACAAATGT-----CAGCCAGCCCTTCTGTGTGTCTCAACAGTCTTC 1236
 QY 2557 GTTCATACCTGATCAAAAGTTTCAAGGCTCGTAATGACATGGGGTTTGGCCCGAGCAG 2616
 Db 1237 GTGCTTATGAGATCAAAAGTTTCAAGGCTCGTAATGACATGGGGTTTGGCCCGAGCAG 1296
 QY 2617 GTAGTCAATGGACATTTCTGAGAGAACCTCCCAATGTGTGCTCTGAGAACGTGTG 2676
 Db 1297 GTCACTATGGCTACTCTGAGAGAGACTACCCCAAGCAATCCTGAGCTGGAAGCAAT 1356
 QY 2677 AATGTGTGAACATGACTTACCCAGGTGCACTGGGACCCAGTACTCTGAAAGATC 2736
 Db 1357 GAAATCTTCACTCAAGTGCCTGTGCTCAAGTGGCGGCTGGAGCTGGCCCAAGTGC 1416
 QY 2737 CGAGACACCTTCAAGGCTATGATGATTTATTTGGAAGACCAAGTTCATCTTAAAGA 2796
 Db 1417 AAGGCGCACCTTCGGGATCAATGTGATGATCTGAGAGAGGAGGAGTGAAGAGCAC 1476
 QY 2797 AACAGACGTCATTTGAGAAAGAAATCTCTCACTTCAAGGAGCAAGACTCATGAGCAT 2856
 Db 1477 AGCAAGAGACATCTCAAAAGACATGATGTGTGTGCGGCAACACACAGTGTCTATC 1536
 QY 2857 TTGCGGGGCTAGAGCCCTTTAGCACTACATGATGATGATGATGATGATGATGATG 2916
 Db 1537 CTCAATGCTTGGGCTTGTATGATGATGATGATGATGATGATGATGATGATGATG 1596
 QY 2917 GGGAGAGGCGCCAGCCCTGACAGAGCTTTATATCTCAGAGAGAGTCCCAAGTGT 2976
 Db 1597 GATGCGGGCCCGCAGC---GAGTTACCTTACACACCCCAAGAGAGTGTGTGCGCAC 1653
 QY 2977 CCTGTCTTTGAAATTTGTAATCTCAACATGATGATGATGATGATGATGATGATG 3036
 Db 1654 CCGAGAGGCTTGAATCTGAGAGTGAATGAAACACCAAGCTGTGTGTGTGTGTGTGT 1713
 QY 3037 CCGAGCCACCCGATGAGATTTTGAACAGATGACCTTAAAGTATCAGCAATTAACAG 3096
 Db 1714 CCATCAGGCAACAGGCGTGTCAACCGCTACGCTCTCTTACACCC-----C 1764
 QY 3097 ACATGATTTAGGCGCTGTGTATTTGAAATTTCTGCGCAACAGACAGGTGAGCT 3156
 Db 1765 CTGATGAGAGGGGAGAGGGGCACTGTCTTCAACTTGGGACCCCGAATTTGGAGA 1824
 QY 3157 TTAATAATTTAAATTTGACATGATTAATTTTATTTATGACAAACATCAGCA 3216
 Db 1825 CACAACTGACCGATCTCAGCCCACTGGGTGATCCGCTTCACTTCAAGCCACAC 1884
 QY 3217 GATCAGAGAGTCAAAATTAACAGAGAGCATGACATGATGATGATGATGATGATG 3276
 Db 1885 AAGAGGGGCGCT-----GGTGAAGCATGTGTAGGGAGAGGACACTA 1927
 QY 3277 CCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3336
 Db 1928 TGGCTTGTGTGGGATCTCAGATTTTGGCAATCTCAGCAACAGCGGTGAAACTCA 1987
 QY 3337 GCTGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3396
 Db 1988 GTGTGTCTCTGT 2045
 QY 3397 AACTTTATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3456
 Db 2046 CAAAGCTTGGAGAGAGAGAGGAGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2097

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QY 3457 AATGTTCTCGAGCTTCTTGGGTTAAAGGCTATGCGAGGAACAGATACAAAGTT 3516
DB 2098 AGCTAACACCAAGAGCTCTTCAACAGAGTGGAGCTGACCTGACCTACACGAGATC 2157
QY 3517 CGAGTTGCTGCTGGGGGAGCTCTGTTTGTGAGTTCAAGAGATGTTTGAAGACAGCC 3576
DB 2158 CACTTGTTAAGAGAGATGTTCCGGACCAATGGCTGTGTAAGACCAATGGACAGAGC 2217
QY 3577 CCAGCATGGAAGCCCGCAGTGGATTTGCACTCAGGGCTGGTTTATGGCTGAGT 3636
DB 2218 CCGGTAGG--CTCCCTCTGCTGGCTTCCAGCTGAGGGCTGTTCATCGGCTTTGTG 2274
QY 3637 TGGTGTGCTGCTCTCTTATCTTAAATTTTGTGCTGATTTGCTTCAACAGAAACAAG 3696
DB 2275 AGTGCATATCTCTCTGCTCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2334
QY 3697 GGTGTAAATATCAGTTAAAGAAAGAAAGATGCCATGCTGACCTGAAATCCAGCTT 3756
DB 2335 GGGCGCAATATCTCAGTGAAGATTAAGAGAGACACCGAGTGAAGCTGAGGCCGAGCC 2394
QY 3757 ATGAAGAAAGATATGAGGACATTTGAGAAATACAGTATGCAAGAACCAAGCCTTG 3816
DB 2395 ATGAAGATGAGACCTTCCGCGAGTACAGTCCCTGAGAGTGAACAAGAGAGAGGCC 2454
QY 3817 AAAAAAGAGTGAAGCTCTCTTCAAGAGCTGTGAAAAAGAAATAGTGAAGAGCAGC 3876
DB 2455 TTGGCAGCAGCCAGCATGCTCAACGCGGAGATCAAGGCCCTGGGACATGACGACAGC 2514
QY 3877 CTAGTGAATGAGAGAGGGGTTAAATGGCAGTTCAATGAGAGTGGCTTTTATTTGA 3936
DB 2515 CTGGCCGATATATGGGGGAGCGTGAATGTTCAATTCAAGAGATGATGTTGCTTATGGC 2574
QY 3937 CATACAGTGTAAAGAAAGAAAGA 3962
DB 2575 CAGTACAGTGGCAAGAGAGAAAGA 2600

RESULT 11
US-08-506-296B-3
; Sequence 3, Application US/08506296B
; Patent No. 6313265
; GENERAL INFORMATION:
; APPLICANT: Phillips, Greg
; APPLICANT: Cunningham, Bruce A.
; TITLE OF INVENTION: NEURITE OUTGROWTH-PROMOTING POLYPEPTIDES
; TITLE OF INVENTION: CONTAINING FIBROBLAST TYPE III REPEATS AND METHODS OF USE
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute
; STREET: 10550 No. 6313265th Torrey Pines Road, TPC-8
; CITY: La Jolla
; STATE: California
; COUNTRY: U.S.
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/506,296B
; FILING DATE: 24-JUL-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: TSRI 488.0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 554-2937
; TELEFAX: (619) 554-6312
; INFORMATION FOR SEQ ID NO: 3:

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 3991 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 59..3859
; US-08-506-296B-3

Query Match 3.8%; Score 157.4; DB 4; Length 3991;
Best Local Similarity 44.2%; Pred. No. 7.3e-36;
Matches 1106; Conservative 0; Mismatches 1266; Indels 129; Gaps 6;

QY 233 AAGACTTGGTACAGCTTCCACCATCACCACAGCTCTCCAAAAGATTACATTATGACC 292
DB 147 ACGATTTCTCGAGCCCGCCGAGCTGACGAGAGAACCCCGGACACATCGTGTCTTCC 206
QY 293 CTGGGAGAAATTGTAAATCCAGTGAAGCAAGAGGAAACCGCCCAAGCTTTCT 352
DB 207 CCAATGATGACATGCTCTCAATATCGTGGCCAGCGGAAACCCCTCTCAATACCAT 266
QY 353 GAGCCGTAATGGAGCTCATTTTGAATGATGAAGACCTCTGTCAACATGAAGCCTG 412
DB 267 GAGAGCTGATGATGATGAGCTTCCGCTTGTCCCGAGAGAGACAGGGGGGCTCCGCTCCG 326
QY 413 GCAAGAAAGCTCATTAATTAATCATCATGATGAGGAAAGGAAAGCTAGACCTATGAAGAG 472
DB 327 GATCGGGGACTTTGTATCAATCAAGCCAGTGGCCGCGGCTCCAG-----GGGC 377
QY 473 TCTATCAGTGTACAGAAAGAGAGAGCGGAGCTGACGTTTCTAATAATTTGTTGCC 532
DB 378 GCTTCGCTCTTCCGACCAAGCGGTTGGGACCGCTGTCTCTCCAGGCGCAACGTCA 437
QY 533 GCCCATCCAGATCACCATTTGTGACCAAAAGAAACCTGAACATCACTTCAAGTG 592
DB 438 TCGCGAGAAACACTCGCAGGTGGCCGAGAGAGAGTGAACCCGGTGAAGTGAAGAG 497
QY 593 GTCACTTTTATGATCTTCCCTGCAAGACCCCAATTTGATTAACCACTTAATATTTT 652
DB 498 GGGACCCCGTGTGTGCTCTGTGAACCCCGAGAGCGCTGTTCCTCTAAATCTATT 557
QY 653 GGATGATATCTCTTTTAAAGCTTCAAAAGTGAAGAGTTTCTCAAGTTGAATG 712
DB 558 GGCTCAACGAGCAATCTTCAATGCTCAGAGAGAGAGGCTCTTATGGGAGAGATG 617
QY 713 GGGACCTTTATTTTCCATGCTCTCCAGAGAGACCCGCGAGACTATATCTGTATG 772
DB 618 GGAACCTTACTTCTCAAGAGCAATGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 677
QY 773 CTAGATTATATATCTCAACCATACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 832
DB 678 CTCACCTCTCGAGCCCGCCAGCATATCAAGAGAGAGAGAGAGAGAGAGAGAGAG 737
QY 833 CAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 892
DB 738 CAGTGAATG----- 746
QY 893 CTAAATCAAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 952
DB 747 -----CGGTTGGTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGAGCA 800
QY 953 AAGAGAAATTAAGAGAAATGCTTCACTGAGAGCTTTCAGAGAGAGAGAGAGAGAGAG 1012
DB 801 CCATGCGCTCCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 860
QY 1013 CATATTTTACTGGGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1072
DB 861 CATGGGTCGATGGCGGCGGCTGAAGCG-----CCCTCTCTCCGCGCGCGGCTTGA 914

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QY 1073 ACTTGAGAAAACCTTGACAGATCATTGTTTACAGAACAGACTCTGAGAAATTACCAAT 1132
 DB ACTTGAGAAAACCTTGACAGATCATTGTTTACAGAACAGACTCTGAGAAATTACCAAT 1132
 DB 915 ACTTGAGAAAACCTTGACAGATCATTGTTTACAGAACAGACTCTGAGAAATTACCAAT 974
 QY 1133 GATATGCAAAAATGATATGAGAGCATTCCACATTCATTTCTGTAAAGTTAAAGCCG 1192
 DB 975 GTGTGCTGAGAAACGGAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1034
 QY 1193 CTCCTACTGATGATCAGAGCCCTTCAAAATCTTGTCTGTCTCCAGAGAGAGAGAGAGAG 1252
 DB 1035 CCCCATATTTGGGTGG 1094
 QY 1253 TGATCTGAGAGCTAATGAGCAACCCCAAAACCAAGATTAGCTGTTTACAAATGAGAGTC 1312
 DB 1095 TGAGACTGAGAGGTGG 1154
 QY 1313 CATATGAAATTTGCTCTGATGACCCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1372
 DB 1155 CCATGAGAGCTCGGG 1211
 QY 1373 CAATGTTCAAGAAAGATCAAGTCAATATGATATGATATGATATGATATGATATGATATGAT 1432
 DB 1212 CGAGAGTGG 1271
 QY 1433 ATTTACTGCAAAACGCAATTTGTAATGTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAG 1492
 DB 1272 CCTATTTGGGCAACGCTTCTGCAAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1331
 QY 1493 CAAACACACTTACCAAGGCTATTTGCAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1552
 DB 1332 ATGAGAGAGCTACAG 1391
 QY 1553 GGTCTCTCTCCCAACCATGAG 1612
 DB 1392 GGG 1451
 QY 1613 ATATTATGTTTACATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAAT 1672
 DB 1452 ACCGATCTCTGTTTACATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAA 1511
 QY 1673 AAGAAATTCCTGTGG 1732
 DB 1512 GGG 1571
 QY 1733 AATTGAGATGAGCAAAAGATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATG 1792
 DB 1572 TGGAGGTGAG 1631
 QY 1793 GAGAGATGAGTCTCTTGAATGCAAAAGTGAATGCAATGATGATGATGATGATGATGATGAT 1852
 DB 1632 GGGAGAGAGTCTCTTGAATGCAAAAGTGAATGCAATGATGATGATGATGATGATGATGAT 1691
 QY 1853 TGTGCTGAG 1912
 DB 1692 TGGAGTGTGAG 1751
 QY 1913 ATCTAGTGTAGTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1972
 DB 1752 AATATGAGTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1811
 QY 1973 CCACTCTGAG 2032
 DB 1812 CCCCTCTGAG 1867
 QY 2033 CAGTCTCCGTTTACATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2092
 DB 1868 TCCCGGAG 1898
 QY 2093 ACAAAGTGTGAG 2152
 DB 1899 AACACCGGTGAG 1958
 QY 2153 TCATATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2212

DB 1959 TGTGTGAG 2018
 QY 2213 TTTTGGAG 2272
 DB 2019 TTTTGGAG 2078
 QY 2273 GGTATGAG 2332
 DB 2079 GGTATGAG 2138
 QY 2333 TGACGAAAGCTTACAG 2392
 DB 2139 AGACCCCGGG 2198
 QY 2393 CTGATATTTGAG 2452
 DB 2199 CCGGAG 2258
 QY 2453 TTCAATGAG 2512
 DB 2259 CCGGAG 2318
 QY 2513 TGGCAATGATCAATATATTTGTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2559
 DB 2319 GGTTCGG 2378
 QY 2560 CCAATCTGATGAG 2611
 DB 2379 GGTTCGG 2438
 QY 2612 CAGCTGATGAG 2671
 DB 2439 GAG 2498
 QY 2672 GTGTGATGAG 2712
 DB 2499 GGTGAG 2539

RESULT 12
 US-08-427-497E-5
 ; Sequence 5, Application US/08427497E
 ; Patent No. 5969124
 ; GENERAL INFORMATION:
 ; APPLICANT: Lemmon, Vance
 ; TITLE OF INVENTION: A Method for Characterizing the
 ; TITLE OF INVENTION: Nucleotide Sequence of L1CAM and
 ; Patent No. 5969124
 ; TITLE OF INVENTION: the Nucleotide Sequence
 ; Characterized thereby
 ; NUMBER OF SEQUENCES: 44
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSER: Fay, Sharpe, Beall, Fagan,
 ; STREET: 1100 Superior Avenue
 ; STREET: Suite 700
 ; CITY: Cleveland
 ; STATE: Ohio
 ; COUNTRY: U.S.A.
 ; ZIP: 44114-2518
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette, 3.50 inch, 720 kb
 ; MEDIUM TYPE: Storable
 ; COMPUTER: Compaq Prolinea 5100e
 ; OPERATING SYSTEM: DOS 5.0
 ; SOFTWARE: ASCII
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/427,497E
 ; FILING DATE: April 24, 1995
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 07/904,991

FILING DATE: June 26, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Minnich, Richard J.
REGISTRATION NUMBER: 24,175
REFERENCE/DOCKET NUMBER: CWR 2 149-3-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (216) 861-5582
TELEFAX: (216) 241-1666
TELEX: (216) 980162
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1794
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: nucleic acids
HYPOTHETICAL: irrelevant
ANTI-SENSE: no
ORIGINAL SOURCE:
ORGANISM: homo sapiens
INDIVIDUAL ISOLATE: 17-18 week fetus
IMMEDIATE SOURCE:
LIBRARY: Stratagene cDNA Library 936206
CLONE: 17
PUBLICATION INFORMATION:
AUTHORS: Hlavín, Mary Louise
TITLES: Molecular structure and functional testing of
TITLE: human L1CAM: an interspecies comparison.
JOURNAL: GENOMICS
VOLUME: 11
ISSUE:
PAGES: 416-423
DATE: 1991
RELEVANT RESIDUES IN SEQ ID NO: 2731 to 4503
US-08-427-497E-5

Query Match 3.6%; Score 148.4; DB: 2; Length 1794;
Best Local Similarity 60.3%; Pred. No. 2,1e-33;
Matches 245; Conservative 0; Mismatches 161; Indels 0; Gaps 0;

QY 3605 TTGCAACTCAGGCGTGTCTGATGTCGTGCTGCTCTCTTACTTAATTT 3664
DB 641 TCSCCACTGAGGCGTGTCTGATGTCGTGCTCTCTCTCTCTCTCTCTCT 700
QY 3665 TGTGATGTTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 3724
DB 701 TGTCTATCT 760
QY 3725 AAGATGCCCATGCTGACCTGTAATCCAGCTTGAAGAAAGTGAAGCAATTGGAG 3784
DB 761 AGACACCCAGGCTGAGCTCTGAGGCCCGACCGATGAAGATGAGCCTTGGGAGTAC 820
QY 3785 AATACAGTATGAGAAAGACACCAAGCTTTGAAAAAGAAAGTGAATCTCTTCAAGCA 3844
DB 821 GGTCCCTGAGAGTGAACAGAGAAAGAGCTTTGGCAGCAGCCATCTCCTCAAGC 880
QY 3845 GGAAGTGAAGAAAGAAAGATGAGACAGCCTTGTGCTATGAGAAAGGGTTAATG 3904
DB 881 GGGACATCAAGCCCTGAGGAGTGAACAGCAGCCTGAGCTATGAGGGGAGAGCTGAGATG 940
QY 3905 GCCAGTTCAATGAGATGAGCTCTTTATGAGCAATCACTGATGTAAGAAAGAAAGAGC 3964
DB 941 TTGAGTTCAAGAGATGATGTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1000
QY 3965 CGGCTGAAGAAAGAAAGAGTCAAGAGCCTTCTCTGTCACAGC 4010
DB 1001 CGGCAAGGAGGAGTGAAGAGCTCAGGGGCACTTCCCATCAACCC 1046

RESULT 13
US-09-621-976-3173/c
; Sequence 3173, Application US/09621976

Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTs and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 1935
SOFTWARE: Patent.pm
SEQ ID NO 3173
LENGTH: 455
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: 128..322
US-09-621-976-3173

Query Match 3.1%; Score 128.2; DB: 4; Length 455;
Best Local Similarity 91.3%; Pred. No. 8.7e-28;
Matches 136; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 2944 GTCTTAATCTCCAGAGAGTCCCAAGTCTCTCTCTTGAAGATTGTGATCCA 3003
DB 240 GACTGTAAGTTCTCACTGTAAGTCCCAAGTCTCTCTCTTGAAGATTGTGATCCA 181
QY 3004 AACTGAGCTCTCTCACTTGAAGATCCAGGACCCGAAATGGATTTGACA 3063
DB 180 AACTGAGCTCTCTCACTTGAAGATCCAGGACCCGAAATGGATTTGACA 121
QY 3064 GAGTACACCTTAAGTATCAGCCCAATTAA 3092
DB 120 GAGTACACCTTAAGTATCAGCCCAATTAA 92

RESULT 14
US-08-427-497E-6
; Sequence 6, Application US/08427497E
; Patent No. 5969124
GENERAL INFORMATION:
APPLICANT: Lemmon, Vance
TITLE OF INVENTION: A Method for Characterizing the
TITLE OF INVENTION: Nucleotide Sequence of L1CAM and
Patent No. 5969124
TITLE OF INVENTION: the Nucleotide Sequence
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fay, Sharpe, Beall, Fagan,
ADDRESSEE: Minnich & McKee
STREET: 1100 Superior Avenue
STREET: Suite 700
CITY: Cleveland
STATE: Ohio
COUNTRY: U.S.A.
ZIP: 44114-2518
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 720 KB
MEDIUM TYPE: Storable
COMPUTER: Compaq Prolinea 5100e
OPERATING SYSTEM: DOS 5.0
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/427,497E
FILING DATE: April 24, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/904,991
FILING DATE: June 26, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Minnich, Richard J.

REGISTRATION NUMBER: 24,175
REFERENCE/DOCKET NUMBER: CMR 2 149-3-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (216) 861-5582
TELEFAX: (216) 241-1666
TELEX: (216) 960162
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 1042
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: nucleic acids
HYPOTHETICAL: irrelevant
ANTI-SENSE: no
ORIGINAL SOURCE:
ORGANISM: homo sapiens
INDIVIDUAL ISOLATE: 17-18 week fetus
IMMEDIATE SOURCE:
LIBRARY: Stratagene cDNA Library 936206
CLONE: C2
PUBLICATION INFORMATION:
AUTHORS: Hlaavin, Mary Louise
AUTHORS: Lemmon, Vance
TITLE: Molecular structure and functional testing of
TITLE: human h1CAM: an interspecies comparison.
JOURNAL: GENOMICS
VOLUME: 11
ISSUE:
PAGES: 416-423
DATE: 1991
RELEVANT RESIDUES IN SEQ ID NO: -26 to 1016
US-08-427-497E-6

Query Match 2.4%; Score 99.8; DB 2; Length 1042;
Best Local Similarity 48.8%; Pred. No. 4e-19;
Matches 303; Conservative 0; Mismatches 312; Indels 6; Gaps 1;

239 TGTACAGCTCCAAACATCAACCAACAGCTTCCTCAAAAGTATTAATGACCTTCGGG 298
118 TGAATGAGCAGCTGTCATCAAGCAAGCTTCACAGGCGCTGTGTCCTCCACAG 177
299 ACAATATTTAATCCAGTGTGAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 358
178 ATGACATCAAGCTCAAGTGTGAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 237
359 GTAATGGAAGCTATTTGACATGATTAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 412
238 GGAATGCTGTCACCTCAACCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 297
413 GCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 472
298 ACTGTCCTTCACATCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 357
473 TCTATCAGTGTACAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 532
358 TCTACCGCTGCTTTCACATCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 417
533 GCCCATCAAGTCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 592
418 TGGCCAGAGGTGCCCCCAAGTGGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 477
593 GTACGCTTTAGTATTCCTTCGAGAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 652
478 GGAAGTCAAGTGTGCTTCGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 537
653 GGATGATATTCCTTCGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 712
538 GATGATCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 597
713 GGAACCTTATTTTTCATGTCCTTCAGAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 772
598 GCAACCTTACTTGTGCAATGTCTCACTCCGACCAAGCAAGCAAGCAAGCAAGCAAG 657

773 CTAGATTATATCACTCAACCAATACAGAGCAAGCAAGCAAGCAAGCAAGCAAG 832
658 CCCACTTCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 717
833 CAGTGTGATGAATGAATGACA 853
718 CCACCAAGCAGATGATGACA 738

RESULT 15

US-08-232-463-14/c
Sequence 14, Application US/08232463
Patent No. 5670367

GENERAL INFORMATION:

APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.

TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52

CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA

COUNTRY: USA
ZIP: 22313-0299

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
FILING DATE:

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:

APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU

TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-9300
TELEFAX: (703) 683-4109
TELEX: 899149

INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: PTZgpt-Fls

US-08-232-463-14

Query Match

Best Local Similarity 1.6%; Score 65.2; DB 1; Length 7218;
Matches 13; Conservative 199; Mismatches 112; Indels 0; Gaps 0;

3665 AGAAGAAAGAGGTGTAAATATCACTTAAGAAAGAGATGCCAGTCAACCT 3744
1365 RRR 1306
3745 GAAATCCAGCTATGAAGAGATGATGAGCAATTTGAGAAATCAGATGAGCAAGAC 3804
1305 RRR 1246
3805 CACAAGCTTTGAAAGAAAGAGTCAAGCTCTTCAGACAGAGCTGTGAAAAAGAGAT 3864

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OM nucleic - nucleic search, using sw model

Run on: May 23, 2004, 02:51:56 ; Search time 1625 Seconds
(without alignments)
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Perfect score: 4134
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Scoring table: IDENTITY NTC
Gapop 10.0, Gapext 1.0

Searched: 295383 seqs, 2272363821 residues

Total number of hits satisfying chosen parameters: 5907676

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq.*
12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
13: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
14: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq.*
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16: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq.*
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18: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
19: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	3233.6	78.2	6384	10	US-09-919-039-279
2	737.2	17.8	4131	16	US-10-161-493-59
3	472.8	11.4	7491	13	US-10-435-751-4
4	472.8	11.4	7491	13	US-10-435-751-151
5	472.8	11.4	7491	13	US-10-435-751-153
6	469.6	11.4	7570	13	US-10-435-751-18
7	469.6	11.4	7570	13	US-10-435-751-193
8	469.6	11.4	7570	13	US-10-435-751-195
9	469.6	11.4	7650	13	US-10-435-751-2
10	469.6	11.4	7650	13	US-10-435-751-152
11	469.6	11.4	7650	13	US-10-435-751-158
12	469.6	11.4	7650	13	US-10-435-751-164
13	469.6	11.4	7650	13	US-10-435-751-170
14	469.6	11.4	7650	13	US-10-435-751-176

15	469.6	11.4	7650	13	US-10-435-751-182	Sequence 182, App
16	469.6	11.4	7650	13	US-10-435-751-188	Sequence 188, App
17	469.6	11.4	7650	13	US-10-435-751-194	Sequence 194, App
18	469.6	11.4	7651	13	US-10-435-751-207	Sequence 207, App
19	445.4	10.8	2662	16	US-10-104-047-78	Sequence 78, App
20	423.6	10.2	7686	13	US-10-435-751-14	Sequence 14, App
21	423.6	10.2	7686	13	US-10-435-751-181	Sequence 181, App
22	423.6	10.2	7686	13	US-10-435-751-183	Sequence 183, App
23	411.6	10.0	7602	13	US-10-435-751-10	Sequence 10, App
24	411.6	10.0	7602	13	US-10-435-751-169	Sequence 169, App
25	411.6	10.0	7602	13	US-10-435-751-171	Sequence 171, App
26	404.4	9.8	7527	13	US-10-435-751-12	Sequence 12, App
27	404.4	9.8	7527	13	US-10-435-751-175	Sequence 175, App
28	404.4	9.8	7527	13	US-10-435-751-177	Sequence 177, App
29	358.4	8.7	7563	13	US-10-435-751-16	Sequence 16, App
30	358.4	8.7	7563	13	US-10-435-751-187	Sequence 187, App
31	358.4	8.7	7563	13	US-10-435-751-189	Sequence 189, App
32	357	8.6	6487	13	US-10-435-751-6	Sequence 6, App
33	357	8.6	6487	13	US-10-435-751-157	Sequence 157, App
34	357	8.6	6487	13	US-10-435-751-159	Sequence 159, App
35	351	8.5	4523	16	US-10-411-010-6	Sequence 6, App
36	351	8.5	4523	16	US-10-411-010-7	Sequence 7, App
37	348.4	8.4	7329	13	US-10-435-751-8	Sequence 8, App
38	348.4	8.4	7329	13	US-10-435-751-163	Sequence 163, App
39	348.4	8.4	7329	13	US-10-435-751-165	Sequence 165, App
40	347	8.4	4192	15	US-10-084-817-343	Sequence 343, App
41	340	8.2	445	9	US-09-864-761-10809	Sequence 10809, A
42	340	8.2	579	15	US-10-029-186-5113	Sequence 5113, A
43	340	8.2	32250	10	US-09-764-891-8315	Sequence 8315, A
44	238	5.8	238	15	US-10-029-186-18869	Sequence 18869, A
45	231.8	5.6	32176	10	US-09-764-891-8316	Sequence 8316, Ap

ALIGNMENTS

RESULT 1
US-09-919-039-279/c
; Sequence 279, Application US/09919039
; Publication No. US20030108871A1
; GENERAL INFORMATION:
; APPLICANT: Kaser, Matthew R.
; TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
; FILE REFERENCE: PA-0035 US
; CURRENT APPLICATION NUMBER: US/09/919,039
; PRIOR APPLICATION NUMBER: 60/222,113
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 401
; SOFTWARE: PERL Program
; SEQ ID NO 279
; LENGTH: 6384
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Inocyte ID No. US20030108871A1 201395.4C
US-09-919-039-279

Query Match 78.2%; Score 3233.6; DB 10; Length 6384;
Best Local Similarity 89.4%; Pred. No. 0;
Matches 3722; Conservative 0; Mismatches 9; Indels 433; Gaps 5;
QY 1 CTTCAAGTTCCTCCGATGAAATTAATCTTAACGTTGACACACACAGCTTCAGAAATCTT 60
DB 5927 CTTCAAGTTCCTCCGATGAAATTAATCTTAAC-TTGCACACACAGCTTCACAAATCTT 5869
QY 61 TTGTAAGAGAGAAAGAAATTCAGTGTGAGTCTCAGCAGAGAGTTAGCTATATGCGAG 120
DB 5868 TTGTAAGAGAGAAAGAAATTCAGTGTGAGTCTCAGCAGAGAGTTAGCTATATGCGAG 5809
QY 121 CTTAAATATGCGCAAGAAAGAGGCTTATCTGCGGCGAGAGTCCCTGATTTCTTC 180

Db 5808 CTTAAATATGCGGAAAAAGAACCGCTTATCTGCGGAGAGAGTGCCTGATTCCTTC 5749
Qy 181 CTGTGCAGATGATTAAGTCACTGGAAGTACCTCTGATCCAAAACCTCTGGAAGACTTG 240
Db 5748 CTGTGCAGATGATTAAGTCACTGGAAGTACCTCTGATCCAAAACCTCTGGAAGACTTG 5689
Qy 241 GTACAGCCTCCCAACCATCAACCAAGCTCTCCAAAAGATTACATTAATGACCTCGGAG 300
Db 5688 GTACAGCCTCCCAACCATCAACCAAGCTCTCCAAAAGATTACATTAATGACCTCGGAG 5629
Qy 301 AATATTGTATCCAGTGTGAAGCCAAAGGAAAACCGCCCCCAAGCTTTCTGTGACCCGT 360
Db 5628 AATATTGTATCCAGTGTGAAGCCAAAGGAAAACCGCCCCCAAGCTTTCTGTGACCCGT 5569
Qy 361 AATGGAGCTATTTGATCATGATTAAGACCTCTGTGTCACATGAAGCTGGCAGAGA 420
Db 5568 AATGGAGCTATTTGATCATGATTAAGACCTCTGTGTCACATGAAGCTGGCAGAGA 5509
Qy 421 ACCTCATATTAATCAATCATGACGGAAGGGAAGCTGAGACCTATGAGAGATCTATCAG 480
Db 5508 ACCTCATATTAATCAATCATGACGGAAGGGAAGCTGAGACCTATGAGAGATCTATCAG 5449
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Db 5448 TGTACAGCAAGAAAGCAAGCGGAGCTGCACTTTCTAATTAACATTTGTTCCGCCATCC 5389
Qy 541 AGATCCCATTTGGAACCAAGAAAAAAGTGAACCATCACTTCAAAAGTGTGCTGCT 600
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Qy 601 TTAGTACTTCCCTGAGAACCCCAATTTGATTAACAACATTAATTTTGGATGAT 660
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Qy 661 AATCTCTTGAAGACTTCCAAAGTGAAGATTTCTCAAGCTTTGAATGGGACCTT 720
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Qy 841 GAATTGAATGACATATAGCTGCTAATTGATGACATGAGTTTATGCTGTAATCA 900
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Qy 901 AGTAGAGAGAGGCAACCAATTTTAACTCGAAGAGCAATGCAAGTAAACAAGAGAA 960
Db 5085 AGTAGAGAGAGGCAACCAATTTTAACTCGAAGAGCAATGCAAGTAAACAAGAGAA 5026
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Qy 1321 ATTGCCCTGATGACCCCAAGCAAGAAATTAATGAGGCTATACATTAATTTTCAAACTT 1380
Db 4665 ATTGCCCTGATGACCCCAAGCAAGAAATTAATGAGGCTATACATTAATTTTCAAACTT 4606
Qy 1381 CAAGAAGATCAAGTGAATATCATGATGCAATGCTCTAATGAATATGATATTTACTG 1440
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Qy 1441 GCAAAAGATTTGTAATGCTGCTGAGCCCAACCAATCTTCAACCTGCAAAACA 1500
Db 4545 GCAAAAGATTTGTAATGCTGCTGAGCCCAACCAATCTTCAACCTGCAAAACA 4486
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Db 4485 CTCTACAGGCTATTTGCAACAGGCTGCTTTACTAGCTGCTCTTTGGGCTCTCT 4426
Qy 1561 CTCCCAACATGAGTGTGTTTAAAGAGCTAAAGAGTGTCTTATGAGATATTTAT 1620
Db 4425 CTCCCAACATGAGTGTGTTTAAAGAGCTAAAGAGTGTCTTATGAGATATTTAT 4366
Qy 1621 GTTTTACATGAAATGGAACCTTTGGAATCAAGATGCTACATGATGTTAAAGAAAT 1680
Db 4365 GTTTTACATGAAATGGAACCTTTG-----GAAATTT 4336
Qy 1681 CCTGTGGCCCAAAAGAGACATTAATGAGTGTGTTGCAAGATTAATTAAGG 1740
Db 4335 CCTGTGGCCCAAAAGAGACATTAATGAGTGTGTTGCAAGATTAATTAAGG 4276
Qy 1741 ATGGCAAGATGAAGTCACTT-----ACAGCCC 1770
Db 4275 ATGGCAAGATGAAGTCACTTAAATCAAGATGCTACATGATGCTTAAACAGCC 4216
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Db 4155 CACACCTTATCCCTCACTGCTCTGTGCTGGAAGACAAAGAGAACTGCCCATGATGA 4096
Qy 1891 AGTTCACTGTGAAGAGATCATCATGATGATGCTGATGCTGATGCTGATGATGACGGG 1950
Db 4095 AGTTCACTGTGAAGAGATCATCATGATGATGCTGATGCTGATGCTGATGATGACGGG 4036
Qy 1951 ACCTCAAGTGTGAGCAACCACTGAGACAGCTCTCCGCAAGCTGTGCTTAC 2010
Db 4035 ACCTCAAGTGTGAGCAACCACTGAGACAGCTCTCCGCAAGCTGTGCTTAC 3976
Qy 2011 GTTGTGCTCTTACCTCACTCACTGCTCCGTTTACATGCTCCCAATCTCTCCCTTAC 2070
Db 3975 GTTGTGCTCTTACCTCACTCACTGCTCCGTTTACATGCTCCCAATCTCTCCCTTAC 3916
Qy 2071 TTAAGATGAGATCACTTGAAGAAAGTGTGAGCTGCTGATGAGACCCAGGCGATGAC 2130
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Qy 2191 CTGTGGACCAACCAATGGAATTTTGAACAACAGACCAAGCCAGCTGAAGTGTCT 2250
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 DB 3495 GATGAATGACATCTGT 3436
 QY 2551 ACCTTTGTTCATCTGATCAAAAGTTCAAGGCTTGAATGACATGGGGTTTGGCCCGAG 2610
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 QY 2911 GGGAAAGGGGAGGCGCCAGCCCTGACAGAGTCTTTAATCTCCAGAAAGAGTCCCT 2970
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 DB 2955 GATCCACCGAGCCAGCCGATTTGAGAGATGACCTTAAAGTATCAGCCAT 2896
 QY 3091 AACAGACACATGATTTAGGCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3150
 DB 2895 AACAGACACATGATTTAGGCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2836
 QY 3151 TGGACTTTAAAAATTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 3210
 DB 2835 TGGACTTTAAAAATTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 2776
 QY 3211 TCAGCAGATCAGAAAGTCAAAATTTACAGAGAAAGCAGTAAACCTGTGATGAAGTGTGT 3270
 DB 2775 TCAGCAGATCAGAAAGTCAAAATTTACAGAGAAAGCAGTAAACCTGTGATGAAGTGTGT 2723
 QY 3271 ATTCTTCAACCTGT 3330
 DB 2722 2723
 QY 3331 CTACTGCTGACAGCTGCTGAGACTATGCAATATCATGTTGGGAATATGAGGACCAAG 3390
 DB 2722 2723
 QY 3391 CATGTAACTTTTATGTGATATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3450

DB 2722 2723
 QY 3451 ATTGTAAATGTGTTCTCGAGCTTCTTTGGGTTAAAGGGCTTAATGCCAGAAACAGATAC 3510
 DB 2722 2723
 QY 3511 AAAGTTGAGTTGT 3570
 DB 2722 2723
 QY 3571 ACAGGCCAGGATGCGCAAGCCGCGAGTGATGATTAATGCACTCAGGCTGTGTTCAATGCT 3630
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 DB 2670 CTGATGT 2611
 QY 3691 AACAGGGGTGTAAATTCAGTTAAAGAAAGAAAGATGCCATGCTGACCTGAATTC 3750
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 QY 3751 CAGCCTTAAAGAAAGATGATGGAATTTGAGAAATACAGTATGACAGAAACCAAG 3810
 DB 2550 CAGCCTTAAAGAAAGATGATGGAATTTGAGAAATACAGTATGACAGAAACCAAG 2491
 QY 3811 CTTTGAAGAAAGAAAGATGCACTCTTCAAGAGACTGTGCAAAAAAGAAATGTGTAC 3870
 DB 2490 CTTTGAAGAAAGAAAGATGCACTCTTCAAGAGACTGTGCAAAAAAGAAATGTGTAC 2431
 QY 3871 GACAGCTTGTGATGATGAGAAAGGGTTAATGCGCAGTTCAATGAGATGCTCTT 3930
 DB 2430 GACAGCTTGTGATGATGAGAAAGGGTTAATGCGCAGTTCAATGAGATGCTCTT 2371
 QY 3931 ATTGACAAATACAGTGTGTGAAAGAAAGAAAGAGCCGCTGAAAGAAAGCTCAAG 3990
 DB 2370 ATTGACAAATACAGTGTGTGAAAGAAAGAAAGAGCCGCTGAAAGAAAGCTCAAG 2311
 QY 3991 GCACTTCTCTGTGTGAAAGCCATGATCTTTGTTAATTTTAAAGTCAAAAGCAATA 4050
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 QY 4051 TTCAATTTCTGAGAAATTTAATCTAGCTCTTGTGTGAGCCCTCATATGATA 4110
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 QY 4111 CATATGGGTAGAGATATATTTTC 4134
 DB 2190 CATATGGGTAGAGATATATTTTC 2167
 RESULT 2
 US-10-161-493-59
 ; Sequence 59, Application US/10161493
 ; Publication No. US2004001855A1
 GENERAL INFORMATION:
 ; APPLICANT: Anderson, David W
 ; APPLICANT: Zernhusen, Bryan D
 ; APPLICANT: Li, Li
 ; APPLICANT: Zhong, Mei
 ; APPLICANT: Gerlach, Valerie
 ; APPLICANT: Shimkets, Richard A
 ; APPLICANT: Gorman, Linda
 ; APPLICANT: Pena, Carol BA
 ; APPLICANT: Kekuda, Ramesh
 ; APPLICANT: Paturajan, Meera
 ; APPLICANT: Spytek, Kimberly A
 ; APPLICANT: Leite, Mario W
 ; APPLICANT: Raabelli, Luca
 ; APPLICANT: MacDougall, John R
 ; APPLICANT: Taupier Jr., Raymond J

Db 1421 TCTTTGGGTCTCCCATCCCACTGCGATGTTTAAAGATGGGCAAGAACCACTCG 1480
 Qy 1607 ATGAGATATTTATGTTTACATGAAATGGAACCTTGGAAATCAAGATGCAATGGA 1666
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 Qy 1667 TCGTTAAAGAAATTCCTGTGGCCCAAAAGACAGTACAGAACTTATAGTGTGCA 1726
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 Db 1600 GTCCGCTGAGGATTAAGAACCCCAACAGATCTACCGATGCGGAGACCAAGTGGCC 1659
 Qy 1786 CAAGAGGAGAGATGTGTCTTGTGAATGCAAGTGAATGATACACCTTATCCCTC 1845
 Db 1660 AGAAGGGGCAACCGGTGCACTGGAGTGTGGGTAAAGCAACACCTCTCCGAAATCTC 1719
 Qy 1846 ACTGTCTGTGGTGAAGACAACAGGAACTGCCAGTATGAAGTTCACTGTTGAC 1905
 Db 1720 ACCGTCTACTGGTGAAGATGACAGCCGCTTATATTGGAACAAGATGAAGAA 1779
 Qy 1906 AAGATCATCTAGTGTAGCTGATGTCACTGACATGACAGCGGACCTACACGTGTG 1965
 Db 1780 GACGACTCCCTGACATCTTTGGGGTGGGAGAGCGGAGACAGGCGAGTTACAGTGTGTC 1839
 Qy 1966 GCGAACAACCTGTGACAGCGCTCCGACAGCGTGTGCTTATGCTGTCTACT 2025
 Db 1840 GCGAGACCGAGATTAACCAAGACTGGCCAGGCTTACCTCACTGTCTAGAGACG--- 1896
 Qy 2026 CCAATCCAGCTCCCGTTACGATGTCCCAATCTCTCTTGACTTGAACGACAGAT 2085
 Db 1897 -----CAAGACCGGCTCCCGGAGCTTGAAGCTGACCGAC 1929
 Qy 2086 CAATTTGACAAAAGTGTGAGCTGTGATGACCCCAAGGACATGACAAATAGCCCAT 2145
 Db 1930 CTGGCGAGAGAGCGTGGCGGTGACCTGATCCCGGGAGATCTAACAAAGCCCCATC 1989
 Qy 2146 ACMAATTTATCATGCAATATGAAATGCAATGCAACAGCGGCTGTGGCAACCA 2205
 Db 1990 ACAGACTACGTGTCTCAAGTTTGAAGAACCAAGTTTCAACTGGGGTCTGGCAATGACAT 2049
 Qy 2206 ACTGAAGTTTGGAAACAGACCAAGCCAGCTGAGCTGTCTTACGTAACGTAAC 2265
 Db 2050 TCCAAATACCCGCGACGCTTAATCTAGCCGTCTCCGCTGTCTCCGTAATGCACTAC 2109
 Qy 2266 TCCCTCCGCTGATGAGCAGTGAACAGATTTGGAGAGGCTTGGCCAGGAGCGCTGAG 2325
 Db 2110 CAGTTCGATGATTCATTCACAGAGTTTGGAGAGCAACCCAGCTCCCATCCGAG 2169
 Qy 2326 CAGTATTTTACGAAAGCTCTGACAGACAGATTAATAAACCACAGCTGTGAGAGATCGGA 2385
 Db 2170 CCTTCCGAAACAGTGAAGACACCCCGGAGTCCAAATCTGTGTGACCTGTGAAGGAGGGG 2229
 Qy 2386 TCAGAGCTGATTAATTTGAGATTAAGTGAAGCCCTTGAATGTTTGAATCTATGAG 2445
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 Qy 2446 CGAGGCTTCAAGTAAAGTTAGCTGCGCCAGAAAGATGATGATGATGATGATCATCT 2505
 Db 2290 CCAACCTGCGTCACTGTGCAAGTGAAGCGGAGAGACATCGAAGGCTGTGAACAC 2349
 Qy 2506 GTGGTTTGGCAATATATCAATATATTTGTCTAGGAGACCGCAACTTTTGTCCATAC 2565
 Db 2350 GTCAAGTGTG---GGGCTCTGCTACGTTGTTGGGAGACCCCACTTACGTCCTAT 2406
 Qy 2566 CTGATCAAGTTTCAAGGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 2625
 Db 2407 GAGATCGAGTCCAGGCTGAAATGACTTCCGGAAGGCGCTGTAGGCAAGTCCGTCATC 2466
 Qy 2626 GGAATTTGAGAGAACCTCCCAATGATGCTCTGTGAGACGTGCTGTGATGTGTGTG 2685

Db 2467 GGTACTCCGAGAAATTAATCCAGGGCTGCGCCACTGAATGAATTAAGTCCAGTATG 2526
 Qy 2686 AACAGTACTTATGCGAGGTGACATGAGACCCAGTACTTGAAGAAAGATCCGAGAAC 2745
 Db 2527 AACAGCAAGCATAGCTTCAATGGAACCGGCTTACTCCGACAGGTCCAGGGCCAG 2586
 Qy 2746 CTACAGGCTATCGAATTTATTAATGGAAGACCCAGATTCATTAAGAAACAGACGT 2805
 Db 2587 CTACAGAGTACCGAGCTTACTGAGAGAGAGACAGCTTGTGTAAGAACCTGTGGGTG 2646
 Qy 2806 CACATTGAGAAATATCTTCACTTCCAGGACCAAGATCTATGAGCATGTTCGGGG 2865
 Db 2647 TCTCAGAAAGACACCAAGCCAGCTTGTGTGACCGCTCCGCTGGGTGTGTGTC 2706
 Qy 2866 CTAGAGCCCTTATGACATCACTGATGATGCGAGTGTCAATGAGGAAAGGAGGCG 2925
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 Qy 2926 CCAGCAGCCCTGACAGAGTCTTTAATATCTCCAGAGAGTCCCGAGTCTCCCTCT 2985
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 Db 2887 CCAATGGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2946
 Qy 3104 -----AATTAAGCCCTCTGTGATGATTTGAATTCCTGCCAAGACAGCGTGG 3153
 Db 2947 AACGGACCAAGTGAAGAGATGAGTGAAGAACTTCTCCCAATCAGACCAAGTTC 3006
 Qy 3154 ACTTTAAATTTAATTTTATGACATGATGATGATGATGATGATGATGATGATGATGAT 3213
 Db 3007 ACGGTGCAAGAACCGAGCCCGGTGTGACGCTTACCTTACCTTACCTGAGCGGAG 3066
 Qy 3214 GCGAGTACAGAAAGTCAATTAACAGAGAGAGTGAACATGATGATGATGATGATGAT 3269
 Db 3067 GTGGCTCTGGGAAACCGGTGACAGAGAGTCAACAGACCCCGAATGAAGTGTG 3122

RESULT 3
 US-10-435-751-4
 ; Sequence 4, Application US/10435751
 ; Publication No. US2004005348A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Agnays, Inc.
 ; APPLICANT: Paris, Mary
 ; APPLICANT: Challita-Bid, Pia M.
 ; APPLICANT: Jakobovits, Aya
 ; APPLICANT: Raitano, Arthur B.
 ; APPLICANT: Ge, Wangmao
 ; TITLE OF INVENTION: Nucleic Acids and Corresponding Proteins
 ; FILE REFERENCE: 51158-20084.00
 ; CURRENT APPLICATION NUMBER: US/10/435,751
 ; PRIOR APPLICATION NUMBER: 60/404,306
 ; PRIOR FILING DATE: 2002-08-16
 ; PRIOR APPLICATION NUMBER: 60/423,290
 ; NUMBER OF SEQ ID NOS: 208
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO. 4
 ; LENGTH: 7491
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (272)...(3787)
 US-10-435-751-4

Query Match 11.4%; Score 472.8; DB 13; Length 7491;
Best Local Similarity 48.8%; Pred. No. 1,1e-128;
Matches 1467; Conservative 0; Mismatches 1507; Indels 30; Gaps 6;

243 ACAGCTCCAAACCATCAACCAAGTCTCCAAAAGATTACATTATTGACCTTCGGAGAA 302
367 ACAGGTTCCAACATCATATAAAGTCAAAAGTTCAGTTCCTTCGATGAGTA 426
303 TATGTATACAGTGGAGGCAAGGAAACGGCCCAAGTTTCTCGACCGGTAA 362
427 TTTTCAATTGAATGAGCTAAAGAAATCCAGAACATTTTCGTGACTAAGAA 486
363 TGGGACTATTTTGACATCGATTAAGACCTCTGTCACCATGAACTGGACAGAAAC 422
487 TGGCAACCTTTTATTTTACGTGACCATGGGATTAATTCATGAAACATTCAGAA----- 541
423 GCTCATTAATTACATCATAGAGGAGGAAAGCTGAGACCTATGAAAGAGTCTATCAGTG 482
542 ---ACATTGAGATCCCAACGAGGGGACATATCTCATCTTCAAGGAAATACCGCTG 597
483 TACAGAAAGAAAGAACGGGAGCTGACGTTCTAATTAATGTTGTCCGCCATCCAG 542
598 CTTTGCTTCAATAAATCTGGGAATCGCTATGCAAGAAATGAATTAATGATTCAG 657
543 ATCAACATTGTGGACCAAGAAAACCTTGAAACCAATCACACTTCAAGTGTGACTCTT 602
658 TGTTCCAAAATTTCCCAAGAAAATTAATGACCTCTTGAAATGAGAGAGAGATCCAT 717
603 AGTACTCTCCCTGAGACCCCAATTGGATTAACCAACCTTAATAATTTTGATGATGA 662
718 TGTCTCCATGCAATCTCTCCAAAGGCTCCCACTTTTACATTTATTTGATGAATAT 777
663 TTTCTTTCAAAAGCTTCCAAAGTGAAGATTTCTCAAGTTTGAATGGGAGCTTTA 722
778 TGAATTAGAACACATGGAACAGATGAAGATGATCARGAGCAAAAGGAGATCTATA 837
723 TTTTTCCAATGTCTCTCCAGAGAGACCCGCAAGACTATATCTGTTATCTGATTTAA 782
838 CTTTCGAAAGCTGGAAGAAAAGAGACAGTCCCAATGACTACTGCTTTCTGCTGCAATTTCC 897
783 TCACTACTCAACCATACAGAGAGAACCTATTTCTGAGAGTGAATTCAGTGAATGA 842
898 AAGATTAGAGACTATGTACAGAAAATGCAATGAAACATTAACAGTTTAAAGAA 957
843 ATTGAATGACATATAGCTGCTAATTTGAGTGAACCTGATTTATGTGCTTAATCAG 902
958 TGTAAATGACTCAAGTTTATCAAGAAATTTGTTCCAAAGCAAAATTCATCAAGCAAG 1017
903 TAGAGAGAGGCCCAACATTTTAACTCCAGAAAGCAATGCAAGTAAACAAAGAGAAAT 962
1018 AAAAACCAACCTGCTGTGCTCCCACTGAGAGTGAAGTCTTCAATTAACATCTCT 1077
963 AAGAGAAATGTGCTTCACTGAGTGCATTTGCAAGAAAGACTGCTTACCCCAATTAATTA 1022
1078 CAAAGGGGAAATCTGCTGCTGAGTGTGTTGCTGAAGGCTTGCCTCAACTCCACAGGTGA 1137
1023 CTGGGCAAGAGATGAGATGCTACCCAAAACAGGACAGTTTATTAAGACTTTGAGAA 1082
1138 TTGGAACAAAATTTGTGTGATCTTACCAAGGAGAGAAAGAAAATTAATATGCA 1197
1083 AACCTTGACATCATTTCTTCAAGAGAGACTCTGAAATTAACAAATGTTATACAA 1142
1198 GACTTTGAAATGAGATGTCTCTACAGAGCAAAAGAAATTAATGCTGCAACAGCA 1257
1143 AAATGATTAAGAGCAATCAACATTAATCTGTTAAGTTAAAGGGCTCCATATCTG 1202
1258 CAATTTCTTGGAAACAGCCACTACGATTTTCAAGTTATGATGAAGAGCTCTCGCTG 1317
1203 GATCAGAGCCCTCAAAATCTTGTGTGCTGCTCCAGAGAGAGATGGAGCTTATCTGCA 1262
1318 GACAAAGAAAGCTCAGAGTGTGTATAGCACCGGAAGCAATGAGATCTTGTATGTGA 1377

1263 AGCTAATGCAACCCCAACCCAGAAATTAAGTGTGTTAACAAAATGATGCCAATAGAAAT 1322
1378 GGCTAAGAGAAAGCTCAACCAACATCAAGTGAAGATCAATGGCTCCCAAGTTGACAA 1437
1323 TGCCCTGATGACCCCAAGGAAAAATGATGGCATACATTAATTTTTCAAAATGTTCA 1382
1438 TCATCAATTTG---CTGGATGATGTTGTTCCCAAGGAAATAGTTTATCAACCTTCA 1494
1383 AGAAATCATAGTGCATATATCACTGCAATGCTCTAATGAATATGATATTTTACTGGC 1442
1495 ACCAATCATACTGCTGTGTACAGTGTGAAGCTCAATGTCCATATGACATATCTTGC 1554
1443 AAAGCAATTTGTAATGTGCTGCTGAGCACCAAGATCTCTACACCTGCAACACACT 1502
1555 CAATGCCAATATTTGATGTTGTGATGTCCTGCTCATTTGATACAAACCAAGATGAGAAA 1614
1503 CTACAGATCATTTGAAACAGGCTGTTTACTAGCTGTGCTTCTTGGGTCTCTCT 1562
1615 TTAGCTACAGTGTGGGTACAGTGTCTTTCATTTGCGAGTCTTGTCTTCACTGA 1674
1563 CCCAACCATCGAGTGTTTAAAGAGCTAAAGAAAGTCTCTTCATGAAAGATATTTATGT 1622
1675 GGCAATGCTGTCTGTGCAAGAGTGAAGAGTGAACCCCTGAGGGCAAGCGGTATCA 1734
1623 TTTACATGAAATGGAATCTTTGAAATCAAGAGTCTACATGATGTTTAAAGAAATTC 1682
1735 TATCTATGAATATGCAATTTGCAATGCAACGAACCAAGAAAGATGCTGGTCTTA 1794
1683 TGTGGCCCAAGAACAGTACAGAACTTTATCGTGTGTTGCAAGAAATTAATGGAT 1742
1795 CTGATGTTGGTGAAGAAATGCTATGAGAAATCTGCAATCAAGCAATTTGATATTA 1854
1743 GGCAAGATGAAAGTTCACTTACAGCCCAATATGCAATTTGCAAAAGAGAGATGAT 1802
1855 AAATGCTCAAAATCTTAAGATTTCTCTTAAGATCTGTATCTCCCAATTTGCAATGCT 1914
1803 GTCTTTGAATGCAAAATGGAACATGATCAACCTTATCTCTGCTGTGCTGA 1862
1915 TGAATTAATCTGTAAGAAAGAAATGATCACTATTTGAAACAGATTTGAAGTTCTCTG 1974
1863 GGAACAAGAGAACTGCCAGTATGAAAGTTCACTGTTGACAGAGATCATCTAGTGT 1922
1975 GAGTAAAGATGAGAGAGCTTTGA-----AATTAATGCAAGAAATGAGAGAT 2025
1923 AGCTGATGCACTGACATGACAGAGGAGCTTACAGTGTGTGCAACACCACTCTGGA 1982
2026 AATTAATGATGAGCTAATTTGACATATCTTAATGTAATTTAGAGACCAAGATTTTA 2085
1983 CAGGCTCTCCGCAAGCTGTGCTTAAAGCTGTGCTCTTCAACTCCAGCTCCGT 2042
2086 CTGCTGTTCAGCTCATACTGCTCTAGACAGTGTCTCCGATA---TAACTCAAGTAACTGT 2142
2043 TTAAGATGCAAAATCTCTCTTTGACCTTGAACATGACAGATCAACTTGAACAAAGGT 2102
2143 TCTTAATGTTCCGATCAACAGAAACCTTCACTTGTGTAAGACAGAAAGAGTGT 2202
2103 TCAGCTGATGAGACCCAGGCGATGACAAACAATAGCCCCCATTAACAAATTCATGCA 2162
2203 TGGCTGACCTGGAAGCTGAGCTGACCAACAGCAATATTAAGAGTATATTTGTA 2262
2163 ATATGAAGATGCAATGACCAAGCCAGGCTGTGSCACACCAACTGAAGTTTCTGGAAC 2222
2263 ATTTGAAGAAACAAAGAAAGCTGGAAGGTGGAGAACTGACCAAGATTCAGAGAA 2322
2223 ACAGACACAGCCAGCTGAGAGCTGTCTTAACTGAATCTACTCTTCCGCTGATAGGC 2282
2323 GAAAACCAAGTTATCTTAATCTTTGCTTCAATTTGTGAGATACAGTTTCAGGGTATAGC 2382
2283 AGTGAACAGCATTTGGAGAGAGTTCACAGAGGAGCTGTGAGAGTATTTGACAGAAAGC 2342
2383 CBTGAACAGATGAGAGAGATGACCTTACAGCCGCTTACAGACATCATGAAACACAGCC 2442
2343 CTGAGAACGATTAACCAACCCCAAGCTGTGGAAGAGCTGGATCAGAGCTGATTAATTT 2402

Db	2443	AGCAGCTCCAGATAGGAATCCACAAACATAAAGGTTCAAGCTCTCAACCCAGGAAT	2502
Qy	2403	GGAGATTAAGTGAAGCCCTTGAATGTTTCGAATCTAATGGGCCAGGCTTCAGTAACA	2462
Db	2503	GATTATTAAGTGGAGCCCTTTGAATTCATGGAGCAGATAGGACCAAGGCTTAGAGTACAG	2562
Qy	2443	AGTTAGCTGGCGCCGAGAAAGATGGTGAATGAATGACATCTTGTTGGTTTGGCAATGT	2522
Db	2553	AGTGAAGCTGGAAAGCCACAGGAGGCCCAAGTGAAGTGGAAAGAAACAGTCAACAACC	2622
Qy	2523	ATCCAAATATATTTGTCTCAGGCAAGCCCAACCTTTGTCATATCTGATCAAAAGTTCAAGC	2582
Db	2622	--ACACATTTGGGGGTGAATGAAGCCCTGTCTGTCTATGCCCTTTATGATGTTCMAAGTCAAGC	2679
Qy	2583	CCYGAATGACATGGGGTTTGCCCCCGAGCCAGCTAGTCAATGGGACATTCGAGAAAGA	2642
Db	2680	TATCAATCAACTAAGATCTGGGCTGAGCCCTCAGTCAATGACTCTCTATTTCTGGAGAAAGA	2739
Qy	2643	CCTCCCAATGGTGGCTCTCTGGGAAAGTGCGTGTGAATGTGGTGAACAGTACCTTAGCCGA	2702
Db	2740	CTATCTGTATACAGCTCCAGTGTATCAATGGGGTGAAGCTTTAAACATACATTTAGTTAA	2759
Qy	2703	GGTGACCTGGAGCCAGTACCTCTGAAAGAATCCGAGAACACTCAAGGCTATCGGAT	2766
Db	2800	AGTATCCTGTGCACAGTTCCAAGAGACAGTATATGACGTCTGAAAGGCTATCAAT	2855
Qy	2763	TTACTATTGGAAGAACCCAGAGTTCATCTAAAGAAACAGAGCTCACTTGAAGAAAGAT	2822
Db	2860	AAATTTGGTGAAGAAACAAAGTCTGTGGATGGAGAAACATCCCAAGAAAGTGAACAT	2919
Qy	2823	CCTCACTTTCCAGGCGACAGACTCATAGCATGTTGCCGGGGCTAGAGCCCTTTAGCCA	2882
Db	2920	TCTAAGATTTTCAGGACAAAGAACTCTGGAATGGTCTTCTCTTAGATGCTTTTAGTGA	2979
Qy	2883	CTACACACTGAATGTCCAGTGTCTAATGGGAAGGGGACCGACAGCCCTGACAG	2942
Db	2980	ATTTCATTTACAGTCTTAGCCTATTACTCTAAAGAGCTGGTCTGAAAGTGAAGCTTAA	3039
Qy	2943	AGTCTTTATATCTCCAGAAAGAGTCCCAAGTGTCCCTGTCTTTGAAGATTTGTAATCC	3002
Db	3040	TATATTTCAAACACAGAAAGAGTACTCGAACAGCAACTTTTCTAAAGTCACTCAAGT	3059
Qy	3003	AACACTGAGCTCTCACTTTGGAAATGGGATCCACCGAACCCGAATGGCAATTTTGAAC	3062
Db	3100	TGATTAAGCACTGCGCACTTTATCTTGGGGAGTACTTAAGAAATTAATTAATGAACTTAAAC	3159
Qy	3063	AGAGTACACCTTAAAGTATCAAGCAATTAACAGCACATGAATTAAGCCCTTGTGTGA	3122
Db	3160	TGGCTATCTTTGCAATATCAGATTAATTAAGACACTACAGAGATTTGAGAAATTAATGA	3219
Qy	3123	TTTGAATAAT---CCTGCCAACAAAGACGGGTGACTTTAAATAATTTAAATTTCAAGAC	3179
Db	3220	TATTAACCTTACAACTCATCAAGCCAGCTGGGCACTCTCAAACTGAAATGCAACTAC	3279
Qy	3180	TCGATATTAAGTTTATTTCTATGCAAAACATCAGACAGATCAGGAAGTCAATTAACAGA	3239
Db	3280	CAAGTACAAATTTCTAGGAGGCTTGCACTTCAAGGGCTGTGGAAGAAACCGATACGGA	3339
Qy	3240	CGAA 3243	
Db	3340	GGAA 3343	

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; APPLICANT: Raitano, Arthur B.
; TITLE OF INVENTION: Nucleic Acids and Corresponding Proteins
; TITLE OF INVENTION: Entitled 282PIG3 Useful in Treatment and Detection of
; FILE REFERENCE: 51158-20084.00
; CURRENT APPLICATION NUMBER: US/10/435,751
; CURRENT FILING DATE: 2003-05-09
; PRIOR APPLICATION NUMBER: 60/404,306
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: 60/423,290
; PRIOR FILING DATE: 2002-11-01
; NUMBER OF SEQ ID NOS: 208
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 151
; LENGTH: 7491
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-435-751-151

Query Match      11.4%; Score 472.8; DB 13; Length 7491;
Best Local Similarity 48.8%; Pred: N.1.le-128;
Matches 1467; Conservative 0; Mismatches 1507; Indels 30; Gaps 6

QY      243  ACAGCTCCACCATCACCACCGTCCTCCAAAGATTAACATTAATGACCCCTGGGAGAA 302
Db      367  ACAGGTTCCACCATCATTAACATGATCAAGTCCCAAGTTCCTTCCTGCATGAGTA 426
QY      303  TATGTATATCCAGTGTGAAGCCAAAGGAAACCGCCCCAAGCTTTTCTGTGACCCGTTA 362
Db      427  TTTTCAATTGAATGTGAAGCTTAAGAAATTCAGAACCAACATTTTGTGTGACTTAAGA 486
QY      363  TGGGACTATTTTGAATGATGAATAAGACCTCTGTGTCAACATGAAGCCTGGCAGAAAC 422
Db      487  TGGCAACCTTTTATTTTCACTGACCATCGATATATTCATCGAACATTCAGAG----- 541
QY      423  GCTCATATTAACATCATGAGGGAAGGGAAGCTGAGACTATGAAGAGTCTATCAGTG 482
Db      542  ---ACATTCCAGATCCCAACGAGGGGACATATCTCATCTTCAAGGAAATATACCGCTG 597
QY      483  TACAGCAAGAGCAAGCAAGCGGAGCTGACGTTCTTAATAACATTTGTGCCGCCATCCAG 542
Db      598  CTTTGCTTCAAAATTAACCTGGGAATCGTATGTCAAGAAATTAAGATTTATAGTCCAG 657
QY      543  ATCAACCATTTGTGACCAAGAAAGAAATCTTGAACCAATCACTTCAAGGTGTCACTTT 602
Db      658  TGTTCAAAATATCCCAAAAGAAATTAATGACCTCTGAAGTGAAGAGGAGATCCAAAT 717
QY      603  AGTACTTTCCTGCGACAGCCGCCAATTGATTAACACCACTTAATATATTTTGGATGATA 662
Db      718  TGTCTCCCTCAATGCAATCTCTCCAAAGGCTCCCACTTTTACACATTTATTTGATATAAT 777
QY      663  TTCCTTCAAGACTTCCACAAAGTGAAGAGTTTCTCAAGGTTTGAATGGGACCTTTA 722
Db      778  TGAATTGAACACATCATGCAACAAAGATGAAGATATACATGAGCCAAAAGGAGATCTATA 837
QY      723  TTTTTCACATGTCTCTCCAGAGGACACCCCGGAAGACTATATCTGTATATGCTGAATTA 782
Db      838  CTTGCGAAACGTGAAGAAAGAAAGGACAGTCGAAAGACTACGTGGCTTTTGTGCAATTC 897
QY      783  TCATATCTCAAAACCATACAGCAAGAAAGCAACTATTTCTGTGAAGGTGATTTCAGTGATGA 842
Db      898  AAGATTAAGGACTATTTGTACAGAAATGTCCAATGAACATAACAGTTAACAGTTAAACA 957
QY      843  ATGATAGACACTATAGCTGTCTAATTTGAGGACACATGATTTTATGCTGAATTAACAG 902
Db      958  TGTATATGACTCAAGTTTATATCAAGAAATTTGTTCCAGGCAAAATTCATCAACAGAAAG 1011
QY      903  TAGAGAGGCGCACCAACATTTTATCTCCAGAAAGGCAATGCAATGTAACAAAGAGAAAT 962
Db      1018  AAAACCCAAATGTCTGTGGCTCTCCACATGAGAGTGGCAGTGAATCTTAATACATCCT 1077
QY      963  AAGAGAAATGTCTTCACTGAGAGTCAATTCGAGAAAGACTGCTTACCCCAATTTATTTA 1022

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Db 1078 CAAGGGGAATCTGCTGCTGAGTGTGTTGCTGAAGGCTTGCCAACTCCACAGGTGA 1137
Qy 1023 CTGGGCAAGAGATGSAATGCTACCCAAAACAGAGAGTTTAAAGACTTTGAGA 1082
Db 1138 TTGGAACAAAATTTGGTGACTTACCAAGGGAGAGAGCAAAAGAAATTAATGGCA 1197
Qy 1083 AACCTTGACATCATCTGTTTCAAGAGCAGACTGTGAAAATTACAAATGATATGCAAA 1142
Db 1198 GACTTTGAAAGATGAGAAATGTCTCCACAGAGCAAGAAATTAATGCTGACAGCCAG 1257
Qy 1143 AAATGATTAAGAGCCATCCACATACATTTCTGTTAAGTTAAAGCGCTCCATATG 1202
Db 1258 CAATTTCTTGGGAAACAGCACTCACATTTTCACTTAATATGAAAGAGCTCTGCTG 1317
Qy 1203 GATCAAGGCCCTCAAAATCTGTGCTGCCAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1262
Db 1318 GAAAGAAAGAGCTCAAGAGTGTGTATAGACAGAGAGAGAGAGAGAGAGAGAGAGAG 1377
Qy 1263 AGCTAATGGCAACCCCAAAACCCAGAAATTAGCTGTTAAACAAATGAGTCCATAGAAAT 1322
Db 1378 GGTGAGAGAGAGATCTCAACCCACATCAAGTGAAGATCAATGCTCCCAAGTTGACA 1437
Qy 1323 TGCCCTGATGACCCCAAGCAAAATATAGTGGCATACCATTAATTTTCAATGTTCA 1382
Db 1438 TCATCCATTTG--CTGGTATGTTGTCTTCCCAAGGAAATCAGTTTAAACCAACCTCA 1494
Qy 1383 AGAAATCAAGTCAAGTATATAGTGAATGCTCTAATGATATGATATGATATTTACTG 1442
Db 1495 ACCAAATCATACCTGCTGTATGACAGTGTGAAGCTCAAAATGTCATAGAACTATCTTGC 1554
Qy 1443 AAAGCATTTGTAATGCTGCTGAGCCACCAACGATCTTCACACTGCAACACACT 1502
Db 1555 CAATGCAATATGATGTTGTGATGTGCGTCAATGATACAAACCAAGATGAGAGAAA 1614
Qy 1503 CTACAGATCATGCAAAAGCGCTGTTTACTAGACTGTGCTTTTGGGTCTCTCT 1562
Db 1615 TTACGCTACAGTGTGGTGTACAGTGTCTTACATGAGATCTTGTGCTTCACTCA 1674
Qy 1563 CCCAACCATGAGTGTGTTAAAGAGCTAAAGAGTGTCTTCAATGAAATATTTATGT 1622
Db 1675 GGGAGTGTGTCTGTGAGAGAGTGAAGAGTGAACCCCTGAGGCGCAGCGGTATCA 1734
Qy 1623 TTACATGAAATGAACTTTGAAAATCAAGATGCTACATGATGTTAAAGAAATTC 1682
Db 1735 TATCTATGAAATGAGCATTTGAGATCAACAGAACCCAGAGAAATGTGGTCTTA 1794
Qy 1683 TGTGGCCCAAGAGACATACAGAACTTATACGTGTGTTGACAGAAATTAATAGGAT 1742
Db 1795 CTATGTTGGTGAATAATGCTATAGGAAATCTGACAGTCAACCAATTTGATATTA 1854
Qy 1743 GGGAAAGATGAGTTCATTAAGCCCGAATATGAGTGTGCAAAAGGGAGCATGT 1802
Db 1855 AAATGCTCAAACTTAAGATTTCTCTAAGAAATCTCGATCCCAATTTGATATGCT 1914
Qy 1803 GTCTTTGAATGCAAGATGAAACATGATCAACCTTATCCCTCACTGCTGTGGCTGA 1862
Db 1915 TGAATTAATGTTGAAAGCAATATGATCAATTTGAAACACAGTTTGAAGTTGCTG 1974
Qy 1863 GGAACAAGGAACTGCTCCAGTATGAAAGTTCATGTTGACAGAGATATCTAGTGT 1922
Db 1975 GAGTAAAGATGAGAAAGCTTTGA-----AATTAATGGCAAGAAATGACAGAT 2025
Qy 1923 AGTGAATGATGAGATGACAGCGGAGCTACAGGTGTGGCCAAACCACTCGAG 1982
Db 2026 AATTAATGATGAGATTAATTTGACATATCTAATGTAATTTTAAGAGCAAGATATTA 2085
Qy 1983 CAGGCTCTCCGCAAGCTGTGCTTACGCTTGTGCTCTACTCAATCCAGCTCCGT 2042
Db 2086 CTGCTGTGACCTCATCTGCTCTAGACAGTGTGCGGATA---TAACTCAATTAATCT 2142
Qy 2043 TTAAGATGCTCCAAATCTCTCTTGACTTAAGATGACAGATCAACTGACAAAGTGT 2102
Db 2143 TCTTAATGTTCCGATCCACAGAAACCTTCACTTGTGAAAGACAGAAACAGAGTGT 2202

Qy 2103 TCAGCTCATGAGACCCAGCGATGACAAATAGCCCATTAACAAATTCATCATGA 2162
Db 2203 TCGCTGACCTGGAGAGCTGAGAGTGAACACACAGCAATTTAGCGATATATGTTGA 2262
Qy 2163 ATATGAAGATGATGACAAAGCCAGGCTGTGCAACCAACAACTGAATTTCTGGAAC 2222
Db 2263 ATTTGAAGAAACAAAGAAAGCTGTGAAGGTGGAGAGACGTACACAGATCCAGGAAA 2322
Qy 2223 ACAGACCAAGCCAGCTGAAGCTGTCTCTTAAGTGAATCTACTCTCCGCGATATGC 2282
Db 2323 GAAACCAAGTATCTTAATCTTGTGCTCAATTTGTGATACAGTTCAAGGCTATAGC 2382
Qy 2283 AGTGAACAGATTTGGAGAGAGCTTCCAGAGAGCGTCTGACAGTATTTGACGAAAG 2342
Db 2383 CGTGAACGAATGAGGAGAGAGTCAAGCTTACAGAGCGTCAAGCATATGAAACACCA 2442
Qy 2343 CTGAGACCAATTAACCCCAACAGCTGTGAGAGACTGGATCAAGCTGATATTT 2402
Db 2443 AGCAGCTCCAGATAGAAATCCACAAACATAGGCTTCAAGCTTCAACCCAGAAAT 2502
Qy 2403 GGAATTAAGTGAAGCCCTTGAATGTTGATCTAATGGGCGAGGCTTCAATGACAA 2462
Db 2503 GATTAATGAAGTGGAGCTTGAATTCATGAGAGAGATGACAGAGCTTGAAGTACAG 2562
Qy 2463 AGTTAGCTGCGCAGAAAGATGTGATGATGATGACATCTGTGTGTGGCAATGT 2522
Db 2563 AGTGAACAGAGCAAGGAGGCCAGTGAAGTGGAGAGAAAGACATCACAAACC- 2621
Qy 2523 ATCCAAATATATGTCTCAGAGCAGCCCACTTTGTTCAATCTGATCAAAAGTTCAAG 2582
Db 2622 --ACAAATGCGGATGATGACGCTGTCTATGCTTATGATGATGATGATGATGATG 2679
Qy 2583 CCTGAATGATGAGGTTTGGCCCGAGCAGCTGTATGATGAGCAATCTGAGAGAA 2642
Db 2680 TATCAATCACTAGATCTGGCTGAGCTTCACTGATGATGATGATGATGATGATGATG 2739
Qy 2643 CCTCCAAATGATGCTCTGAGAAAGTGTGATGATGATGATGATGATGATGATGATG 2702
Db 2740 CTATCTGATATAGCTCCAGTATCATGAGGATGATGATGATGATGATGATGATGATG 2799
Qy 2703 GGTGACCTGAGCAACCAATCTCTGAAAGATCCGAGACATCAAGGCTATAGAT 2762
Db 2800 AGTTACTGTGTCAACAGTCTCAAGAGACAGTATGATGATGATGATGATGATGATG 2859
Qy 2763 TTAATTAAGAGACCAAGTGTATCTAATAAGAAACAGATGATGATGATGATGATG 2822
Db 2860 AATGATGAGAAACAAAGTGTGTGATGAGAAACATCTCCAAAGAGTGAACAT 2919
Qy 2823 CCTCACTTCAAGGAGAGACATGATGATGATGATGATGATGATGATGATGATGATG 2882
Db 2920 TCTAATGATTTGAGAGCAAGAAACCTGGAATGATGATGATGATGATGATGATGATG 2979
Qy 2883 CTACACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2942
Db 2980 ATTTCAATTAACAGTCTTGAAGCTTATTAAGAGATGATGATGATGATGATGATG 3039
Qy 2943 AGCTTTTAATCTCAGAGAGAGTCCCAAGTGTGATGATGATGATGATGATGATGATG 3002
Db 3040 TATATTTCAACACAGAGAGATGATGATGATGATGATGATGATGATGATGATGATG 3099
Qy 3003 AACACTGACCTCTCACTTTGAAATGGATCACCGAGCCACCGAATGGCATTTGAC 3062
Db 3100 TGATTAAGACACTGCACTTATCTTGGGAGCTTACTTAAGAAATTAATGAGAACTTA 3159
Qy 3063 AAGATACACTTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3122
Db 3160 TGGCTATCTTTGCAATATCAATATTAATACACTTACGAGATTTGAGATTAATGA 3219
Qy 3123 TTTGAAATTT---CTGCAACAAAGACAGGAGCTTTAAATAATTAATTTAGAGAC 3179
Db 3220 TATTAACATTAACATCTCATTAAGCCAGCTGAGCACTTCAACCTGAATGACATAC 3279

423 GCTCATATTAATCATATGAGCGAAGAAAGCTGAGACCTATGAGAGTCTATGATG 482
462 ----AATTCAGAGATCCCAAGAGAGGCGACATATCTCACTTTCAGAGGAAATACCGCTG 517
483 TACAGCAAGAAAGAAAGCGAGAGCTGCAAGTTCTTAATTAACATTTGTCGCCCATTCAG 542
518 CTTTGCTTCAAAATTAATCTGGGAATCGCTATGTGCAAGAAATGAATTTATAGTTCCAG 577
543 ATCACCATTTGTGAGCCAAAGAAAATTTGAACCAATCAACACTTCAGAGTGTCACTT 602
578 TGTTCCTCAAACTCCCAAGAAAATTAAGACCTCTTGAAGTGAAGAGAGATCAAT 637
603 AGTACTTCCCTGAGAGACCCCAATGATTAACACCACTTAATTAATTTGATGATGA 662
638 TGTCTCCCATGGAATCTTCCCAAGGCTCCCACTTTACATTTATTTGATGAATAT 697
663 TTCTCTTCAAAAGCTTCAACAAAGTGAAGATTTCTCAAGTTTGAATGGGAGCTTTA 722
698 TGAATTTGAACACATGGAACAGATGAAGATATCATGAGCCAAAGGAGATCTATA 757
723 TTTTTCATGTCTCCCAAGAGACCCGCGAAGCTAATCTGTATGCTAGATTTAA 782
758 CTTTCGAAACGTGAAGAAAGAGACGTGCAATGACTATGCTTGTGCTGATTTCC 817
783 TCATACTCAAACTACAGACAGAGCAACCTATTTCTGGAAGGTGATTTCACTGATGA 842
818 AAGATTAAAGACATTTGTACAGAAATGCAATGAATCTAACAGTTTAAGCA 877
843 ATTGAATGACACTATAGCTGTATATTGAAGTGAACCTGAGTTTATGTGCTAAATCAAG 902
878 TGTATATGACTCAAGTTTCATCCAAGAAATTTGGTTCAAGGCAAAATTCATCAAGCAAA 937
903 TTAGAGAGAGCCCAACATTTTTCATCCAGAAAGCAATGCAAGTAACAAAGAAAT 962
938 AAAACCCAACTGCTGTGCTCTCCCAAGAGTGAAGTCTTCAATTAACATCCT 997
963 AAGAGAAATGTGCTTCACTGAGAGTCAATGCAAGAGACTGCTTACCCCAATTTTA 1022
998 CAAGGGGAAATCTTGTCTGCTGAGTGTGTTGCTGAAGCTTCCCACTCCACAGTTGA 1057
1023 CTGGGCAAAAGAAATGAAATGCTACCAAAACAGAGACGTTATTAAGAACTTTGAGAA 1082
1058 TTGGAACAAATTTGGTGTGACTTACCAAGGGGAGAGAAACAAAGAAATTAATGGCA 1117
1083 AACCTTGCAGATCATTTGTTTCAAGACAGACTTGGAAATTTACCATGTTATAGCA 1142
1118 GACTTTGAAGATGAAGAAATGTCTCTTACAGAGCAAAAGAAATTAATGCTGACAGCCAG 1177
1143 AAATGATTAGAGCATTCACCATATCATTTCTGTTAAGTTAAAGGGCTCCATATCG 1202
1178 CAATTTCTTGGAGAACGCACTACGATTTTCACTTTATAGTAAGAGAGCTCTCTGCTG 1237
1203 GATCAAGCCCTCAAAATCTTGTGCTGTCCCAAGAGAGATGGAGCTTATCTGAG 1262
1238 GACAAAGAAAGCTCTAGAGTGTGTATAGCAACCGGAACCAATGGCATTTGTTATGTA 1297
1263 AGCTAATGGCAACCCCAACCCAGAAATTTAGCTGTGTTAACAATTGAAGTCCCAATGAAT 1322
1298 GGTGAAGAGAACTTCAACCAATCAATGAAGAGTCAATGGTCTCCCAAGTTGACAA 1357
1323 TGCCTGTGATGACCCAGAGAAAATAGATGGCGATACCATTAATTTTTCAAATGTTA 1382
1358 TCATCATTTG---CTGTGATGTTGTCTTCCCAAGGAAATCAAGTTTTCACAACTTCA 1414
1383 AGAAAGATCAAGTCAATATCATGCAATGCTTAAATGAATATGATATTTTCTGCG 1442
1415 ACCAAATCATACGTGCTGTACAGTGAAGCTTCAATGTCTCATGAAATCATCTTCC 1474
1443 AAACGATTTGTAATGTGCTGTGAGAGCAACGAATCTTCAACACTGCAAAACACT 1502
1475 CAATCCAAATATGATGTTGTGATGTGCTGCTCATTTGATCAAAACCAAGATGAGAAA 1534

1503 CTACAGGTCATTTGAAACAGGCTCTTTACTAGCTGTGCTTCTTGGTCTTCTCT 1562
1535 TTACGCTACAGTGTGGGTAGAGTCTTCTTCAATGCGAGTCTTCTTGGCTTCACTGA 1594
1563 CCCAACATGAGTGTGTTTAAAGAGCTTAAGAAAGTGTCTTCAATGAAGATTTATGT 1622
1595 GGCAGTGTGTCTCTGAGAGAGTGAAGAGTGAACCCCTGAGAGGCGAGGTATCA 1654
1623 TTACATGAATATGAACTTTGAAATCAAAATGCTATCATGAGATGTTTAAAGAAATTC 1682
1655 TATCTATGAATATGACATTCAGATCAACGAACCCAGAAAGATGCTGGCTTTA 1714
1683 TGTGCCCCAAAGACAGTACAGAACTTATACGTGTGTGCAAGAAATTAATTTGGAT 1742
1715 CTATGTTGGTGAAGAAATGCTATGAAAGAACTGCAAGTCAAGCAATTTGATATTAAG 1774
1743 GGCAGAAATGAAGTTCACTTACAGCCGGAATATGCAAGTTTGCAGAAAGGAGCAATGT 1802
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1895 GAGTAAAGATGAGAAAGCTTTGA-----AATTAATGCAAGAAAGATGGAGAT 1945
1923 AGCTATGTCAGTACATGACATGACAGCGGACCTTACAGTGTGTGCCAACACACTGTGA 1982
1946 AATTATTTAGTGAAGTGAATTTGACCATATCTATATTAATTTAGAGAGCAAGATTTTA 2005
1983 CAGGCTCCCGCAGCGCTGTGCTAGAGTGTGCTCTCTCACTCCAGCTCCGCT 2042
2006 CTGCTGTGACTCATCTGCTTGAAGAGTGTCCGATA--TACTCAAGTAACTGT 2062
2043 TTACGATGTCCCAATTCCTCTCTTGAATGAACTGACAGATCAACTTGAACAAAGTGT 2102
2063 TCTTATATGTTCCGATTCACCAAGAAACCTTCACTGTGTGAAGACAGAAAGATGT 2122
2103 TCACTGTGATGACCCCAAGGATGACAAATAGCCCATTTACAAATTCATATGCA 2162
2123 TCGGCTGACCTGGGAAGCTGAGCTGACACCAACAGCAATTTAGCGATATATTGTTGA 2182
2163 AATGAAGATGAATGACCAAGCCAGCGGTGTGAGCAACCAATGAAGTTTCTGAGAC 2222
2183 AATTGAAGAAACAAAGAAAGCTTGAAGGTGGAAGAACTGACCAAGATCCAAAGAA 2242
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2283 AGTGAAGCAATTTGGAAGAGCTTGCACAGAGGCTGTGAGAGTATTTGACGAAGC 2342
2303 CGTGAAGCAAGTGAAGAGAGTCAAGCTTACAGCCGTACAGCAATATGAACACCAAC 2362
2343 CTGCAACCAATTAACCCCAAGCTGTGGAAGAGATGGATGAGAGCTGATTAATTT 2402
2363 AGCAGCTCAGATGAAGATTCACAAACATTAAGGTTTAAGCTCTTCAACCAAGAAAT 2422
2403 GGAGATTTAGTGAAGCCCTTGAATGTTTGAATCTATGGGCGAGGCTTCAATGACAA 2462
2423 GATTATTAAGTGGAGCTTTTGAATTCATGAGAGAAATGGAACAGGCTTATGATGACG 2482
2463 AGTATGCTGGCGCCAGAAAGTGTGATGATGATGACATCTGTGTGTGCAATGT 2522
2483 AGTGACTGGAAGCCACAGGAGCCCGAGTGAAGGGAAGAAAGACATCACAAAC- 2541
2523 ATCCAAATATATGTCTCAGAGCAAGCCCACTTTGTTCCATCTGATCAAAAGTTGACGC 2582
2542 --ACATTTGGGGGATGAGCGCTGTCTATGAGCCCTTATGATGATGCAAGGTCAGGC 2599
2583 CTTGAATGACATGGGTTTGGCCCGAGCCAGCTGTATGTCATGGGACATTTCTGAGAAAG 2642

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Db 2660 CTATCTCTGATACAGCTCCAGTATCCATGGGGTGGAGCTTATTAACAGTACATTA 2719
Qy 2703 GGTGACCTGGAGCCAGTACCTCTGAAAGATCCAGAGACCTTACAGGCTATCGAT 2762
Db 2720 AGTACTCTGTCACAGCTTCCAAAGACAGAGTACATGACCTTGAAGGCTATCAGAT 2779
Qy 2763 TTAATAATGAGAGACCCAGAGTTCATTAAGAGAAACAGAGCTCATTTGAGAAAAAGT 2822
Db 2780 AATATGCTGAGAAACAAAAAGTCTGTGATGAGAAACACATCCCAAGAGTGAACAT 2839
Qy 2823 CCTGACCTTCCAGAGAGACAGCTATGAGCAGTGGGCTGAGAGCCCTTAGCCGA 2882
Db 2840 TCTAAGATTTTCAGGACAAAGAACTCTGGAATGTTCTTCTTGAATGCTTTAGTGA 2899
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Db 2900 ATTTCATTTAAGCTCTTTCAGCTATTAATCTTAAGAGAGCTGTGCTGAAAGTGAAGCTTA 2959
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Qy 3003 AACACTGAGCTCTCTCACTTTGGAATGGATCCACCGAGCCACCCGAATGGCACTTTGAC 3062
Db 3020 TGAATAAGACACCTGCACTTTATCTTGGGACCTAAGAAATTAATGAGAACTTAAC 3079
Qy 3063 AGAGTACACTTAAAGATATCAGCAATTAACAGACACATGAATGAGCCCTGCTGTAGA 3122
Db 3080 TGGCTATCTTTGCAATATCAGTATTAATGACACCTAGAGATTGAGAAATTAATGA 3139
Qy 3123 TTTGAAATTT---CCTGCCAACAAGACAGGTGACTTTAAATAATTTAATTCAGCAC 3179
Db 3140 TATTACATTTACAACTCCATCAAGGCCAGCTGACCTCTCAACCTGAATCACTAC 3199
Qy 3180 TCGATTAAGTTTATTTATTCATGACAAACATAGAGATGAGAGTCAATTAACA 3239
Db 3200 CAAGTACAAATCTTACTTGAAGGCTTGCACTTCAAGGGCTGTGAGAAACCATCGGA 3259
Qy 3240 GGAA 3243
Db 3260 GGAA 3263

RESULT 7
US-10-435-751-193
; Sequence 193, Application US/10435751
; Publication No. US2004005348A1
; GENERAL INFORMATION:
; APPLICANT: Agensys, Inc.
; APPLICANT: Faris, Mary
; APPLICANT: Chalita-Bid, Pia M.
; APPLICANT: Jakobovits, Ava
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Ge, Wangmao
; TITLE OF INVENTION: Nucleic Acids and Corresponding Proteins
; FILE REFERENCE: 5158-20084.00
; CURRENT APPLICATION NUMBER: US/10/435,751
; PRIOR FILING DATE: 2003-05-09
; PRIOR APPLICATION NUMBER: 60/404,306
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: 60/423,290
; PRIOR FILING DATE: 2002-11-01
; NUMBER OF SEQ ID NOS: 208
; SOFTWARE: PatSeq for Windows Version 4.0
; SEQ ID NO 193
; LENGTH: 7570
; TYPE: DNA
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; ORGANISM: Homo sapiens
US-10-435-751-193
Query Match 11.4%; Score 469.6; DB 13; Length 7570;
Best Local Similarity 48.8%; Pred. No. 1e-127;
Matches 1465; Conservative 0; Mismatches 1509; Indels 30; Gaps 6;

Qy 243 ACAGCCTCCAAACCATACCCCAAGCTCTCAAAAGATTATTAATGACCTCTGGAGAA 302
Db 287 ACAGGTTCCAAACATATTAACAGTCAAAAGTCCAAATGGCTTCCCTTGATGATGA 346
Qy 303 TATTGTAATCCAGTGTGAAGCCAAAGGAAACCGCCCAAGCTTTCTCTGACCCGTAA 362
Db 347 TTTTCAAAATGTAATGTAAGCTAAAGGAAATCCAGAACCAATTTGTGTGACATGA 406
Qy 363 TGGGACTATTTGACATGATTAAGACCTCTGCTGACATGAGACCTGGACAGAAC 422
Db 407 TGGCAACCTTTTATTTTCACTGACATCGATTAATTCATCGAACATTCAGGA---- 461
Qy 423 GCTCATTAATTAATCATATGAGAGGAGAAAGCTGAGACTATGAGAGTCTATCAGTG 482
Db 462 ----ACATTCAGGATCCAAAGAGGGGACATATCTCATCTTCAAGGAAATACCGCTG 517
Qy 483 TACAGCAAGAAACGAGCGGAGCTGCACTTTTAATAACATTTGTTCGCCCATCCAG 542
Db 518 CTTCCTTCAATAATAAATGGGAAATGCTATGTCAGAGAAATAGAAATTAATAGTTCAG 577
Qy 543 ATCACAATTTGAGACCAAGAAATCTGAACCATACACTTCAAAATGGTCAAGTCTTT 602
Db 578 TGTTCATTAATCTCCCAAGAAATTAAGTACCTCTTGAAGTGGAGAGGAGATCCAT 637
Qy 603 AGTACTCTCCGACAGACCCCAATGATTAACACCACTTAATTAATTTGGATGATGA 662
Db 638 TGTCTCTCCATGATCATCTCCCAAGGCTCCCATCTTACACATTAATTTGGATGAAT 697
Qy 663 TTTCTTTCAAGACTTCAACAAAGTGAAGTCTCAAGTGTGAATGGGACCTTTA 722
Db 698 TGAATTAAGACATATGCAACAAAGATGAATGATATATGAGCCAAAGGGAGATCTATA 757
Qy 723 TTTTTCCAATGCTCCCAAGAGACACCGGAGAAACATATATCTGTATGCTAGATTAA 782
Db 758 CTTCGCAACGTCGAGAGAAAGAGACATGCAATGACTACTGTGCTTTCGTCATTC 817
Qy 783 TCATATCAACCATATACAGAGAACCACTAATTTCTGTGAAGTGAATTCAGTGAATGA 842
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Qy 843 ATGATGACACTATAGCTGTAATTTGATGACACTGATTTATGCTGCTTAATCAAG 902
Db 878 TGTCTATGACTCAATGATCCACAGAAATGCTTCCAGGCAAAATTCATCAACCAAG 937
Qy 903 TAGAGAGAGCCACCAACTTTTAACTCCAGAGCAATGCAATTAACAAAGAAAT 962
Db 938 AAAACCCCAATGCTGTGCTCCCTCCACTGAGAGTGGAGTGTCTTCAATTAACATCCT 997
Qy 963 AAGAGAAATGCTTTTCACTGAGTGCATGTCAGAGAGACTGCTTACCCCAATTAATTA 1022
Db 998 CAAGGGGAAATCTTGCTGCTTGAAGTGTGTAAGAGCTTGCACATCCACAGATTGA 1057
Qy 1023 CTGGCAAGAGAAATGTAATGCTTACCAAAAAACGACAGTTATTAAGAACTTTGAGAA 1082
Db 1058 TTGGAACAAATTTGTGTGACTTACCAAGGGGAGAGAAACAAAGAAATTAATGAGCA 1117
Qy 1083 AACCTTGACATCATTTATGTTTCAAGACAGACTCTGGAATTAACATGATATGCAAA 1142
Db 1118 GACTTTGAAGATAGAAATGCTCTTACAGAGCAAAAGAAATTAATGCTGACAGCAG 1177
Qy 1143 AATGATTAAGAGGATCCACATACATATTTCTTGAAGTAAAGGGCTCATACTAG 1202
Db 1178 CAATTTCTTGGAAAGACATCAAGATTTTACATTAATGTAAGAGAGCTCTCGCTG 1237
Qy 1203 GATCAAGCCCTCAAAATCTTGTGCTGTCCCAAGAGAGATGGACCTTGATTCGAG 1262
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Db 1238 GACAAAGAAAGCTCAGAGTGTGTATAGACCCGGAAGCAATGSCATCTTGTATATGA 1297
 Qy 1263 AGCTAATGGCAACCCCAACCCAGATTAAGTGTAAACAAATGAGTCCCATAGAAAT 1322
 Db 1298 GGTGAAGAGAACTCAACCCCAACATCAAGTGAAGATGATGCTCCCAAGTTGACAA 1357
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 Db 1358 TCATCATTTG---CTGTGATGTGTCTTCCCAAGGAATCAGTTTACCAACTTCA 1414
 Qy 1383 AGAAGATCAAGTCAAGTATATCAATGCAATGCTTAATGAATATGATATTACTGCG 1442
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 Qy 1443 AAACGATTTGTAATGTGTGCTGAGCAACCAAGATCTTCACACCTGCAAAACACAT 1502
 Db 1475 CATATGCAATATTGATGTGTGTGATGCTGCTCATTTGATACAAACCAAGATGAGAA 1534
 Qy 1503 CTACAGATCATTTGCAACAGGCTGCTTTACTAGATGCTGCTTCTTGTGCTCTCT 1562
 Db 1535 TTACGCTACAGTGTGGGTAGACGTCTTTCTTAACATGCGATTTCTTGTCTTCACTGA 1594
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 Qy 1683 TGTGCCCCAAAGACAGTACAGAACTTATACGTGTGTGCAAGAGATTAATTAAGGAT 1742
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 Db 1775 AATGCTACAAACTTGAAGTCTTCTTAAGATCTCTATCTCCCAATTCATATGCT 1834
 Qy 1803 GTCTTTGATGCAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATG 1862
 Db 1835 TGAATTTACATGTAAGAAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATG 1894
 Qy 1863 GGACAAACAGAGAACTGCGAGTATGAAAGTTCATGTTGCAAGAGATCATCTAGTGT 1922
 Db 1895 GAGTAAAGATGAGAAAGCTTTGA-----AATTAATGCGACAGAAAGATGAGAGAT 1945
 Qy 1923 AGCTGATGTCAGTGAAGTGAAGAGCGGAGCTTACAGTGTGTGCGCAACCACTCTGA 1982
 Db 1946 AATTATTTGATGAGCTAATTTTGAACATATCTAATGTAATTTTGAAGGACCAAGTATTTA 2005
 Qy 1983 CAGCGTCTCCGCGACAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2042
 Db 2006 CTGCTGTTCAGCTCATATGCTCTTACAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2062
 Qy 2043 TTACAGATGCTCCCAATCTCTCCCTTTGACTTGAATGCTGACAGATCAACTTGAACAAAGTGT 2102
 Db 2063 TCTTATGTTTCCGATCTCAACAGAAACCTTCACTTGTGTGAAGACAGAAACAGAGTGT 2122
 Qy 2103 TCAGTGTTCATGAGACCCGAGGAGTGAACAAATAGCCCATTTACAAATTCATATGCA 2162
 Db 2123 TCGGCTGACCTGGAGAGCTGAGAGTGAACAAACAGCAATTTAGGAGATATATTGTGA 2182
 Qy 2163 AATTAAGATGCAATGCAACAGCCGAGGCTGTGCAACCAACTGAAGTTTCTGGAAC 2222
 Db 2183 AATTGAAGGAAACAAAGAGAGCTGGAAGGTGGAAGGAACTGACCGAGTCCAAAGGAA 2242
 Qy 2223 ACAGACCAAGCCAGCTGAAGCTGTCTCTTACGTAATCTCTCTTCCGCTGATGAG 2282
 Db 2243 GAAACCAAGTATATCTTACCTTGTGCTCATTTGTGAATACAGATTCAGGCTCATAGC 2302
 Qy 2283 AGTGAACAGATTTGGAGAGAGCTTGGCCAGCAGAGGCTGTGAGAGTATTTTGAAGAAC 2342
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Qy 2343 CTGAGAACAGATTAATAAACCACAGCTGTGGAAGAGCTGGATGAGACCTGATTAATTT 2402
 Db 2363 AGCAGCTCAGATTAAGATTCACAAACATAGAGTTCAAGCTCTCAACCAAGGAAT 2422
 Qy 2403 GGAGATTAAGTGAAGCCCTTGAATGTTTGAATCTAATGAGGCAAGGCTTCAATCA 2462
 Db 2423 GATTAATAAGTGGAGCTTTGAATTCATGAGAGAGATGAGACAGGCTTGAAGTCAAG 2482
 Qy 2463 AGTATGCTGGCCGAGAAAGATGATGATGAATGACATCTGTGTGTGTGTGTGTGTGTGT 2522
 Db 2483 AGTGAACCTGGAAGCAAGAGAGGCCAGTGAAGTGAAGAGAAAGAACATCAAAACC- 2541
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 Qy 2643 CCTCCCATAGTGTCTCTGGGAAGTGTGTGTGAATGTGTGAACATTACTTACCGCA 2702
 Db 2660 CTATCTGATACAGCTCAGATGATCATGAGGCTGAGCGTTTAAACAGTACATTAAGTTAA 2719
 Qy 2703 GGTGACTGGGACCCAGTACCTCTGAAAGATCCGAGAGACATCAAGGCTATCGAT 2762
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 Db 2780 AATTTGTGGAAGAAACAAAGATCTGTGATGAGAAAGAACATCCCAAGAAAGTGAACAT 2839
 Qy 2823 CCTGACTTCCAGGACAGACATCATGATGATGTGCGGAGCTTGAAGCCCTTTAGCA 2882
 Db 2840 TCTAAGATTTTCAAGACAAAGAACTCTGGAATGTTCTTCTTGAATGCTTTTGAAGTGA 2899
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 Db 2900 AATTATTTTAACAGTCTTATAGCTTATACCTTATACCTTATACAGAGTGTCTTGAAGTGAACCTTA 2959
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 Qy 3123 TTTGAAATTT---CCTGCAACAGACAGGCTGACTTTAAATAATTTAAATTTTCAAGAC 3179
 Db 3140 TATTAACATTAACATCATCAAGCCAGCTGAGACTCTCAACCTGATGACATCAAC 3199
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RESULT 8
 US-10-435-751-195
 ; Sequence 195, Application US/10435751
 ; Publication No. US20040053348A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Agensys, Inc.
 ; APPLICANT: Farris, Mary

APPLICANT: Challita-Bid, Pia M.
APPLICANT: Jakobovits, Aya
APPLICANT: Raitano, Arthur B.
APPLICANT: Ge, Mangao
TITLE OF INVENTION: Nucleic Acids and Corresponding Proteins
TITLE OF INVENTION: Entitled 2821g3 Useful in Treatment and Detection of Cancer
FILE REFERENCE: 51158-20084.00
CURRENT APPLICATION NUMBER: US/10/435,751
CURRENT FILING DATE: 2003-05-09
PRIOR APPLICATION NUMBER: 60/404,306
PRIOR FILING DATE: 2002-08-16
PRIOR APPLICATION NUMBER: 60/423,290
PRIOR FILING DATE: 2002-11-01
NUMBER OF SEQ ID NOS: 208
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 195
LENGTH: 7570
TYPE: DNA
ORGANISM: Homo sapiens
US-10-435-751-195

Query Match 11.4%; Score 469.6; DB 13; Length 7570;
Best Local Similarity 48.8%; Pred. No. 1e-127; Indels 30; Gaps 6;
Matches 1465; Conservative 0; Mismatches 1509;

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287 ACAGCTCCACCATCATAAAGCTCAAAAGTCAAGTTCCTTCCTTGATGAGTA 346
303 TATTTAATCCAGTGTGAAGCCAAAGGAAACCGCCCAAGCTTTCCTGACCCGTA 362
347 TTTTCAATTAATGTAAGCTTAAGGAATCCAGAACCAATTTTCGTGACTAAGA 406
363 TGGGATCTATTGATGATGATAAGACCTCTGCTGACCACTGACCTCGACAGAAC 422
407 TGGCAACCTTTTATTTTATTCATGACCATGGAATTTTCAATGAAATTCAGGA 461
423 GCTCAATTAATCATCATGAGAGGAAAGCTGAGACCTATGAGAGTCTATCAGT 482
462 ----ACATTCAGATTCCTCAACGAGGAGCAATCTCATCTTCAAGGAAATACCGCTG 517
483 TACAGCAAGAAAGAAAGGAGAGCTGCAAGTTCCTAATTAATTTGTCCTCCCATCAG 542
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1023 CTGGCAAAAGAAAGTGAATGCTACCCAAAAAGAGACGTTTATGAATCTTGAGAA 1082
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1083 AACCTTGAGATCATTTCAATGTTTCAAGAGAGACTCTGAAATTTCAATGATAGCAAA 1142
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1178 CAATTTCTTGGAAAGCACTACGATTTTCAAGTTTATAGTAAGAGAGCTCTCGCTG 1237
1203 GATCAGAGCTCTCAAAATCTTGTCTGCTCCCAAGAGAGATGGAGCTTATGTGAG 1262
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1263 AGCTAATGCAACCCCAAGACCAAGATTAAGCTGTTAACAATGAGATCCCAATGAAAT 1322
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1358 TCATCATTTTGG---CTGGTGAATGTTGCTTCCCGAGAAATCAAGTTTACCACTTCA 1414
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1415 ACCAATCATATGCTGTGTACAGAGTGAAGGCTCAATGTCATGTAATCTTCTGTC 1474
1443 AAACCATTTGTAATGCTGCTGAGCCACCAAGATCTCACACCTGCAACACACT 1502
1475 CAATCCATATTTGATGTTGATGATGTCCTGCTCATGTTATCAACCAAGATGAGAAA 1534
1503 CTACAGATCATTTGCAACAGGCTGCTTATCATGATGTCCTTCTTGGTCTCTCT 1562
1535 TTAAGCTACAGTGTGAGGATACAGTCTTTCTTATGATGAGGCTTTTGGCTTCACTGA 1594
1563 CCCAATCATGAGTGTGTTAAAGAGCTTAAGAGAGTCTTCTCATGAAATTTATGT 1622
1595 GGCAGTGTGCTCTGCAAGAGTGAAGAGTGAACCCCTGAGGAGGAGGCTATCA 1654
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1655 TATCTATGAAATGCAATTTGAGATCAACAGAACCAAGAGAGATGCTGGTCTTA 1714
1683 TGTGCCCCAAAGACAGTACAGAACTTATACGTGTGTCAGAGAAATTAATGAGAT 1742
1715 CTATGTTGGGTAGAAATGCTATAGAAAACTGACATGACAGCCCAATTTGATATTA 1774
1743 GGCAGAAATGAGTTTCACTTACAGCCGGAATATGCAATTTGCAAAAGAGAGATG 1802
1775 AATGCTCAAACTTAAGATTTCTTCAAGATCTGTAATCCCAATTTGATATCT 1834
1803 GTCCTTGAATGCAAGTGAACATGATCACACTTATCCCTGACTGCTGCTGCTGA 1862
1835 TGAATTTAATTTGAAAGCAATGAGTCACTCATTTGAAACAGAGTTGAAAGTGTCTG 1894
1863 GACAAACAGGAACTGCCAGTGAAGAAAGTTCACTGTGACAGAGATCATATGAGT 1922
1895 GATTAAGATGAGAGAGCTTTGA-----AATTAATGACAGAGATGAGAGAT 1945
1923 AGCTATGTCAGTACATGACAGGAGGACCTACACGTGTGTGCGCAACACACTGTG 1982
1946 AATTAATGAGGATTAATTTGACATATCTAATGTAATTTAGAGGACCAAGATTTTA 2005
1983 CAGGCTCTCCGACAGGCTGCTGCTTGAAGCTTGTCTCTCACTCCACAGCTCCCGT 2042
2006 CTGCTGTCAGTCACTGCTCTGAGACAGTGTGCGCAT---TAACTCAAGTAACTGT 2062
2043 TTACAGATGCCAAATCTCTCTTGAATGAACTGACAGATCAACTTGACAAAGTGT 2102

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Db      2063 TCTTGAATGTTCCGATTCACACGAAAACTTCTGCTGTGAAGAAGACAGAACGAGAGTGT 2122
      2103 TTAGCTGTATGAGACCCCGAGGCGATGACAAACATAGCCCATTAACAAATTTATCATCTGA 2162
      2123 TGGCTGACCTTGGAGAGCTGAGCTGACCAACACAAATTTAGGAGATATTTGTGA 2182
      2163 ATATGAGATGCAATGACACAGCCAGGCGTGTGGCACCACCAATGAAATTTCTGGAAC 2222
      2183 ATTTGAGAGAAACAAAGAGAGCTTGGAAAGTGGAGAACTGACAGAGTCCAGAGAA 2242
      2223 ACAGACCACAGCCGAGCTGAGAGCTGTCTCTTAAGTAACTACTCTTCCGCGTATGCG 2282
      2243 GAAACACACAGTATCTTACCTTTGGCTCCATTTTGGAAATACAGATTCAGGGTCAATAC 2302
      2283 AGTGAACACATTTGGAGAGAGCTTGGCCAGGCGGTCTGAGCAGTATTTGACGAAAC 2342
      2303 CGTGAACGAGTAGGAGAGAGTCAAGCTTACGCGGTAGACCATCATGAAACACACACC 2362
      2343 CTCAGAACGAGTAAACACCCACAGCTGTGAAAGGATCGGATCAGAGCTGATATTT 2402
      2363 AGCAGCTCCAGATGAGATTCACAAACATAGAGTTCAAGCTCTCAACCCAGAGAAAT 2422
      2403 GAGATTTACGTGAGAGCCCTTGAATGTTTGAATCTAATGCGCCAGGCTTCAATGACA 2462
      2423 GATTTAAAGTGGAGACCTTTGAAATCCATGAGCAGAAATGACAGGCGCTAGAGTACAG 2482
      2463 AGTTAGCTGCGCCGAGAAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 2522
      2483 AGTGAACCTGGAAGCCACAGGAGGCCCAAGTGAAGTGAAGAAAGAAACAGTACAAACC- 2541
      2523 ATCCAAATATATTTGTCTCAGGACCGCCCACTTTGTTCCATACCTGATCAAAAGTTAGGC 2582
      2542 --ACACATGCGGGGTATATACCGCTGCTGTATGCTGCTTATGATGATCAAGGTCCAGGC 2599
      2583 CCTGAATGACATGGGGTTTCCCGCCGAGCAGCTGATGATGATGATGATGATGATGATGAT 2642
      2600 TATCATCAACTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2659
      2643 CCTCCCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2702
      2660 CTATCTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2719
      2703 GGTGACCTGAGGACCCGATCCTCTGAAAGCATCCGAGGACCTTCAAGAGGCTATGAT 2762
      2720 AGTTACTTGTGATCAAGCTTCCAAAGGACAGATGATGATGATGATGATGATGATGATGAT 2779
      2763 TTACTATTGGAAGACCCAGAGTTTCACTTAAAGAAACAGACGTCATTTGAGAAAGAT 2822
      2780 AATTTGGTGAAGAAACAAAGTCTGTGATGAGAAACACATCCCAAGAGTGAACAT 2839
      2823 CCTGACCTTCCAGGACGACATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2882
      2840 TCTAAGATTTTCAAGGACAAAGAACTCTGGAATGTTCTTCTTCTTCTTCTTCTTCTTCT 2899
      2883 CTACACACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2942
      2900 ATTTCAATTAACAGTCTTACCTTAACTCTTAAAGAGCTGTGCTGAAAGTGAAGCTTAA 2959
      2943 AGCTTTTAACTCTCCAGAGAGTCCCGAGTCTCCCTGCTTTGAAATGATGATGATGATGAT 3002
      2960 TATATTTCACACGAGAGAGTACTTGAACGACCACTTTTCTTAAAGTATCAAAAT 3019
      3003 AACACTGAGCTCTTCACTTTGGAATGGAATGATGATGATGATGATGATGATGATGATGAT 3062
      3020 TGTAAAGACACTGACCACTTATCTTTGGGAGCTACTTAAAGATTTAAATGAGAAACTTAAC 3079
      3063 AGAGTACACTTAAAGTATCAGCAATTAACGACACATGATGATGATGATGATGATGATGATGAT 3122
      3080 TGGCTATCTTTTGAATATCATGATTAATGATGATGATGATGATGATGATGATGATGATGAT 3139
      3123 TTTGAAATTT---CCTGCCACAGACACGCTGAGCTTTTAAATTTAAATTTTCAGCAC 3179

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Db      3140 TATTAACTTACAACTTCATCAAGCCAGCTGAGCAGCTTCAAACTGATGCAACTAC 3199
      3180 TCGATATAGATTTTATTTCTATGACAAACATCAGCAGATCAGAGATCAATTAATACAGA 3239
      3200 CAAGTACAAATTTCTTCTGAGGCTTGGACCTTGCATTCACAGGCTGTGTGAAAAACGATCAGGA 3259
      3240 GGAA 3243
      3260 GGAA 3263

RESULT 9
US-10-435-751-2
; Sequence 2, Application US/10435751
; Publication No. US20040053348A1
GENERAL INFORMATION:
APPLICANT: Agensys, Inc.
APPLICANT: Paris, Mary.
APPLICANT: Chailita-Bid, Pia M.
APPLICANT: Jakobovits, Aya
APPLICANT: Raitano, Arthur B.
APPLICANT: Ge, Wangmao
TITLE OF INVENTION: Nucleic Acids and Corresponding Proteins
FILE REFERENCE: 51158-20084.00
CURRENT APPLICATION NUMBER: US/10/435,751
PRIOR APPLICATION NUMBER: 60/404,306
PRIOR FILING DATE: 2002-08-16
PRIOR APPLICATION NUMBER: 60/4423,290
PRIOR FILING DATE: 2002-11-01
NUMBER OF SEQ ID NOS: 208
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 7650
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (272)...(3946)
FEATURE:
NAME/KEY: misc_feature
LOCATION: 320
OTHER INFORMATION: SNP = C/T = v.9
FEATURE:
NAME/KEY: misc_feature
LOCATION: 668
OTHER INFORMATION: SNP = C/T = v.10
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1178
OTHER INFORMATION: SNP = A/G = v.11
FEATURE:
NAME/KEY: misc_feature
LOCATION: 3484
OTHER INFORMATION: SNP = C/T = v.12
FEATURE:
NAME/KEY: misc_feature
LOCATION: 4615
OTHER INFORMATION: SNP = G/A = v.13
FEATURE:
NAME/KEY: misc_feature
LOCATION: (0)...(0)
OTHER INFORMATION: Pos.: 5078; SNP = C/T = v.15
FEATURE:
NAME/KEY: misc_feature
LOCATION: (0)...(0)
OTHER INFORMATION: Pos.: 5530; SNP = T/A = v.16
NAME/KEY: misc_feature
LOCATION: (0)...(0)
OTHER INFORMATION: Pos.: 5812; SNP = C/T = v.17
FEATURE:

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NAME/KEY: misc_feature
LOCATION: (0)...(0)
OTHER INFORMATION: Pos.: 6114; SNP = A/G = V.18
FEATURE:
NAME/KEY: misc_feature
LOCATION: (0)...(0)
OTHER INFORMATION: Pos.: 6229; SNP = C/T = V.19
FEATURE:
NAME/KEY: misc_feature
LOCATION: (0)...(0)
OTHER INFORMATION: Pos.: 6383; SNP = G/A = V.20
FEATURE:
NAME/KEY: misc_feature
LOCATION: (0)...(0)
OTHER INFORMATION: Pos.: 6626; SNP = C/T = V.21
FEATURE:
NAME/KEY: misc_feature
LOCATION: (0)...(0)
OTHER INFORMATION: Pos.: 6942; SNP = C/T = V.22
FEATURE:
NAME/KEY: misc_feature
LOCATION: (0)...(0)
OTHER INFORMATION: Pos.: 7085; SNP = C/T = V.23
FEATURE:
NAME/KEY: misc_feature
LOCATION: (0)...(0)
OTHER INFORMATION: Pos.: 2684; SNP = A/G = V.24
FEATURE:
NAME/KEY: misc_feature
LOCATION: (0)...(0)
OTHER INFORMATION: Pos.: 3705; SNP = T/C = V.25
OTHER INFORMATION: Pos.: 5768; SNP = T/C = V.26
OTHER INFORMATION: Pos.: 6125; SNP = C/T = V.27
OTHER INFORMATION: Though these SNP variants are shown separately,
OTHER INFORMATION: they can also occur in any combinations and in any
OTHER INFORMATION: of the transcript variants listed in Figures 2A -
US-10-435-751-2

Query Match 11.4%; Score 469.6; DB 13; Length 7650;
Best Local Similarity 48.8%; Pred. No. 1.1e-127;
Matches 1465; Conservative 0; Mismatches 1509; Indels 30; Gaps 6;

243 ACAGCTCCACCATCACCACAGCTCCCAAGATTACATATTGACCTCGGAGAA 302
367 ACAGCTCCACCATCACCACAGCTCCCAAGATTACATATTGACCTCGGAGAA 426
303 TATTTGATTCAGTGTGAAGCCAAAGGAAACCGCCCAAGCTTTTCTGACCCGTA 362
427 TTTTCAATTTGATGTGAAGCTTAAGAAATCCAGAACCAATTTTCTGACCTAAGA 486
363 TGGAGCTCATTTTGAATGATTAAGACCTCTGTCACCATTAAGCTCGACAGAAAC 422
487 TGGCAACCTTTTATTTTCACTGACCATGGATTAATTCATGCAATTCAGAA----- 541
423 GCTCATTAATTACATCATGAGCGAAGGAAAGCTGAGACCTATGAGAGAGTATCAGTG 482
542 ----ACATTCAGATGCCCAAGGAGGACATATCTCATCTTTCAAGGAAATACCGCTG 597
483 TACAGCAAGGAAAGAAAGCGAGAGCTGCAAGTTCTTAATTAACATTTGTGCGCCATCAG 542
598 CTTTGTCTTAATTAATCTGGGAATCGTATGTGCAAGAAATAGAAATTAATGATTCAGAG 657
543 ATACCATTTGTGACCAAGAAATTTGAACCAATCAGCTTCAAAAGTGTGATGCTTT 602
658 TGTTCACAAAATCTCCCAAGAAATTAAGTACCTCTTGAAGTGAAGAGGAGATCCAAAT 717
603 AGTACTTCCCTGAGAGCCCAATTTGATTAACCAACCTATATATTTTGTGATGATTA 662
718 TGTCTTCCATGAGATCTTCCAAAGGCTCCCACTTTACATTTATTTGATGATTAAT 777
663 TTTCTTTCAAGATTTCCAAAGTGAAGATTTTCTCAAGGTTTGAATGGGAGACCTTTA 722

778 TGAATTTAGAACATCGAACAGATGAAGAGTATATCATGAGCCAAAGGAGATCTATA 837
723 TTTTCCATGCTCTCCAGAGAGACCCGGAGACTATATCTGTTATGCTAGATTTAA 782
838 CTTGCAAAAGTGTGAAGAAAGAGACGTGCAATGATCTACTGTTGCTTGTGCAATTTCC 897
783 TCATCTCAAAACCATACAGCAAGAACCACTATTTTCTGTGAAGTGAATTTCAATGATGA 842
898 AAGATTAAAGACTATTTGTACAGAAATGCAATGAACTAAACAGTTTAACAGTTTAACCA 957
843 ATTGAATGACACTATAGCTGTATTTATGAGCACTGAGTTTATGAGTGTAAATCAAG 902
958 TGTCTATGACTCAATTTATCTACAGAAATGTTTCAAGGCAATTCATCAACCAAG 1017
903 TAGAGAGAGCCACCAACATTTTAACTCCAGAGGCAATGCAAGTAAACAAAGAAAT 962
1018 AAAACCCAACTGCTGTGCTCCCACTGAGAGTGGAGTGTGATTTCAATTCATCTCT 1077
963 AAGAGAAATGTCTTTCACTGAGAGTGCATTCAGAGAGACTGCTTACCCCAATTTATTA 1022
1078 CAAGGGGAAATCTGTGCTGTGAGTGTGTTGCTGAAGGCTTGCCCACTCCACAGTTGA 1137
1023 CTGGCAAAAGAAATGTAATGCTACCCAAAACGACAGCTTTATTAAGACTTTGAGAA 1082
1138 TTGAAACAAATTTGTGTGATCTTACAAAGGGAGAGAAACAAAGAAATTAATGCGAA 1197
1083 AACCTTGAGATCATTCATGTTTGAAGAGAGACTCTGAAATTTCAATGATATGACAA 1142
1198 GACTTTGAAGATGAGAAATGCTCTCTTACAGAGACAAAGAAATTTCTGCTGACAGCAG 1257
1143 AAATCATTTAGAGGACCATTCACCATATCAATTTCTGTGAAGTTAAAGGCTCTCATCTG 1202
1258 CAATTTCTTGGAGACAGCACTCAGATTTTCACTTATGAGAAAGAGCTCTCGCTG 1317
1203 GATCAGAGCCCTCAAAATTTGTGCTGTGCTCCAGAGAGAGATGGGACTTTGATGAG 1262
1318 GACAAAGAGCTCTGAGAGCTGTATGACACCGGAAAGCAATGCACTTTGTTATGGA 1377
1263 AGCTAATGGCAACCCCAACCCAGATTAAGTGTATTAACAAATGAGAGTCCCAATGAAT 1322
1378 GGTGAGAGAGAACTCAACCAACATCAAGTGAAGATGATGCTCCCAAGTTGACAA 1437
1438 TCATCATTTG---CTGTGATGTTGTCTTCCAGGAAATCAATTTTATCAACCTTCA 1494
1323 TGCCCTGATGACCCCAAGAGAAATGAGTGGATACCATTAATTTTCAATGTTCA 1382
1383 AGAAATGATCAAGTGAATATCAAGTGAAGTCCCTAATGAATATGATATTTACTGGC 1442
1495 ACCAATCATATCTGCTGTGTACAGTGTGAAGCTTCAATGTCATGAACTATCTTGC 1554
1443 AAAGCATTTGTAATGTGCTGCTGAGCACACGAAATCTCACACCTGCAACACACT 1502
1555 CAATGCCAATATTTGATGTTGTGATGATGCTGCTCATATGATCAACAAAGATGAGAA 1614
1503 CTACAGGCTATTTGAAACAGGCTGTTTACTAGACTGTGCTTTTGGTCTCTCT 1562
1615 TTAAGCTACAGTGTGTTGGGTACAGTCTTTCTTAATTTGCGAGTTCTTTGCTTCACTGA 1674
1563 CCCAATCATGAGTGTGTTAAAGAGCTTAAGAGAGTGTCTTCAATGAAGATTTATGCT 1622
1675 GGCAGTGTGTCTGTGCAAGAGGTGAAGAAATGAAACCTTGAGAGGCGAGGTATCA 1734
1623 TTTTACATGAATATGAACTTTGGAATCAAAATGCTACATGATGCTTTAAAGAAATTC 1682
1735 TATCTATGAATATGCACTTTGCAATCAAGAAACACCGAAGAAATGCTGGGTCTTA 1794
1683 TGTGCGCCAAAGACAGTACAGAACTTATACGTGTGTGCAAGAAATTAATTAAGGAT 1742
1795 CTATGTTGGTGAAGAAATGCTATGAGAAACCTGACAGTCAAGCAATTTGATATTAAG 1854
1743 GGCAAAGATGAATGCTCACTTACAGCCGGAATATGCAATTTGTGCAAGAGAGATGCT 1802
1855 AATGCTACAAACCTTAAGATTTCTTAAGAACTCTGTATCTCCCAATTTGCAATGCT 1914

QY 1803 GTCTTGAATGCAAGTGAATCATATCACACCTTATCCCTCAGTGTCTGTGGCTGAA 1862
 |||||
 Db 1915 TGAATTAACATTTGGAAGAAAGTAATGTGACTACATTTGAAACAGATTTGAAGTTGCTG 1974
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 QY 1863 GGAACAACAGGGAATCTGCCAGTATGAAAGGTTCACTGTTGACAAAGATCATCTAGTGGT 1922
 |||||
 Db 1975 GAGTAAAGATGGAAGACCTTTGA-----AATTAAATGGCAGAAATGGCAGAGT 2025
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 QY 1923 AGCTAGTGTGAGTGAAGTGAAGTGAAGGAGGAGTCACTAGCTGTGTGCGCAACCACTCTGGA 1982
 |||||
 Db 2026 AATTATGATGTGAGCTTAATTTGACATATCTAATGTATGTAATCTTGAAGAGCAAGATTTTA 2085
 |||||
 QY 1983 CAGGCTCTCCGAGGAGGCTGTGTGCTTGTGCTTCTACTCTCACTCAGCTCAGCTCCGT 2042
 |||||
 Db 2086 CTGCTTTGAGCTCATCTGCTCTAGACAGTGTCTGCCGAT---TAACTCAATTAATCTGT 2142
 |||||
 QY 2043 TTAAGATGTCCCAATCTCTCTTTGACTTGAATGACAGATCAACTTGAACAAAGTGT 2102
 |||||
 Db 2143 TCTTGTGTGTCCGAGATCCACAGAAACCTTCACTGTCTGAAAGACAGAAACAGAGTGT 2202
 |||||
 QY 2103 TCAGCTGTATGAGACCCGAGCGATGACAAATATACCCCATTAACAAATTCATCTCA 2162
 |||||
 Db 2203 TGGCTGACCTGGGAAGCTGAGACTGACCAACACCAATATTAGAGATATATTTTGA 2262
 |||||
 QY 2163 ATATGAAGATGCAATGACACAGGAGGAGGCTGTGGACCAACCAACTGAAGTTTCTGGAAC 2222
 |||||
 Db 2263 ATTTGAAGAGAAACAAAGAGAGGCTGGAAGTGGAGAGAACTGACAGAGTCCAAAGAA 2322
 |||||
 QY 2223 ACAGACCAAGCCAGCTGAAGCTGTCTCTTAAGTGAATCTACTCTTCCGCTGTATGC 2282
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 Db 2323 GAAACACAGATATCTTACCTTGTGCTCCATTGTGAGATACAGTTCAGGCTGTATAG 2382
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 QY 2283 AGTGAACAGATTTGGGAAGAGCTTGGCCAGGAGGCTGTGAGCAGTATTTGACGAAGC 2342
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 Db 2383 CGTGAACGAGTAGGAGAGAGTCAAGCTGTAGCCGCTGACAGCAATCATGAAACACACAC 2442
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 QY 2343 CTCAGAACGATTAATAAACCCCACTGTGGAAGAGCTGGATCAGAGCTGTATATTT 2402
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 Db 2443 AGCAGCTCCAGATGAGATTCACAAACATTAAGGTTCAAGCTTCCAAACCAAGAAAT 2502
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 QY 2403 GGAGATTAACGTGGAAGCCCTTGAATGTTTGAATCTAATGTGGCCAGGCTTCACTACA 2462
 |||||
 Db 2503 GATTATTAAGTGGAGACTTTTGAATTCATGAGAGAGAAATGAGCCAGGCTTGAAGTACAG 2562
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 QY 2463 AGTTAGCTGGCCGAGAAAGATGTGATGATGATGATGATGATGATGATGATGATGATGAT 2522
 |||||
 Db 2563 AGTGAACCTGGAAGCCACAGGAGGCCCAAGTGGAGTGGAGAAAGAAACAGTCACAAAC- 2621
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 QY 2523 ATCCAAATATATTTGTCTCAGAGCAGCCCACTTTGTTCCATACCTGATCAAAAGTTAGGC 2582
 |||||
 Db 2622 --ACACATTTGGGGGTATATACCCCTGTCTGTATGCTTATGATGTCAAGGTTCCAGGC 2679
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 QY 2583 CCTGAATGACATGGGGTTTCCGCCGAGCCAGCTGTAGTCAATGGAACATTTCTGGAGAGA 2642
 |||||
 Db 2680 TATCAATCACTAGAGATCTGGGCTGTACCTCAGTCAAGTCACTCTATTTCTGGAGAGA 2739
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 QY 2643 CCTCCCAATGTGGCTCTCTGGGAAGCTGTGTGATGTGTGATGTGTGATGTGTGATGTGTG 2702
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 Db 2740 CTATCTGTATACAGCTCCAGTATTCATGTGGGGTGGAGCTTATTAACAGTACATTTAGTTTA 2799
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 QY 2703 GGTGACCTGGAGCCGATCTCTGAAAAGCATTCGAGAGACCTTACAGAGGCTATGGAT 2762
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 Db 2800 AGTTACTGTGTCAACAGTTTCCAAAGACAGAGTACATGAGACGCTTGAAGAGCTATAGAT 2859
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 QY 2763 TTAATAATGGAAGACCCAGAGTTTCAATTAAGAAACAGAGCTCACTTGAAGAAAGAT 2822
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 Db 2860 AATATGTGTGAAAACAAAAGTCTGTGTGATGGAAGAAACATCCAAAGAGTGAACAT 2919
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 QY 2823 CCTCAGCTTCAAGAGCAAGATCTATGTGATGTGTGCGGGGCTTGAAGCTTTTAGCCA 2882
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 Db 2920 TCTAAGATTTTCAGGACAAAGAACTGTGAATGTGTCTTCTCTTGAATGCTTTTAGTGA 2979
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QY 2883 CTACACACTGAATGTCCGAGTGTGATGAGGAAAGGGAGGGCCAGCCAGCTTGACAG 2942
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 Db 3040 TATATTTCAAAACCAAGGAGGAGTACTGAAACAGCCACTTTTCTAAGGTCAATCAAGT 3099
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 QY 3003 AACACTGAGCTCTCACTTTGGAATGGATCAACGAGCCACCCGAATGGCAATTTGAC 3062
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 Db 3100 TGATTAAGACACTGCGCACTTTATCTTGGGACTTACTTAAGAAATTAATGAAACCTTAAC 3159
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 QY 3063 AGAGTACACCTTAAGATATACCAATTAACAGCAACATGATTAAGGCTCTGTGATA 3122
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 Db 3160 TGGCTATCTTTTGCAATATCAATATATTAATGACACTAGAGATTTGAGAAATTAATGA 3219
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 QY 3123 TTTGAAATTT---CTGCCAACAAGACAGCTGTGACTTTAAATAATTTAATTTAGCAC 3179
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 Db 3220 TATTAACATTAACACCTCAATCAAGCCAGCTGGGACCTTCAAACTGAAATGCAACTAC 3279
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 QY 3180 TCGATATAGTTTATTTCTATGACAAACATCAGAGATGAGAGTCAATTAACAG 3239
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 Db 3280 CAAGTACAAATTTCTATGAGGCTTGGCACTTCAAGGCTGTGAAAAACGATCAAGCA 3339
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 QY 3240 GGAA 3243
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 Db 3340 GGAA 3343
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RESULT 10
 US-10-435-751-152
 ; Sequence 152, Application US/10435751
 ; Publication No. US20040053348A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Agensys, Inc.
 ; APPLICANT: Paris, Mary
 ; APPLICANT: Chailita-Bid, Pia M.
 ; APPLICANT: Jakobovits, Aya
 ; APPLICANT: Ralceno, Arthur B.
 ; APPLICANT: Ge, Wangmao
 ; TITLE OF INVENTION: Nucleic Acids and Corresponding Proteins
 ; FILE REFERENCE: 51158-20084.00
 ; CURRENT APPLICATION NUMBER: US/10/435,751
 ; PRIORITY FILING DATE: 2003-05-09
 ; PRIOR APPLICATION NUMBER: 60/404,306
 ; PRIOR FILING DATE: 2002-08-16
 ; PRIOR APPLICATION NUMBER: 60/423,290
 ; PRIOR FILING DATE: 2002-11-01
 ; NUMBER OF SEQ ID NOS: 208
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 152
 ; LENGTH: 7650
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-10-435-751-152

Query Match 11.4%; Score 469.6; DB 13; Length 7650;
 Best Local Similarity 48.8%; Pred. No. 1.1e-127;
 Matches 1465; Conservative 0; Mismatches 1509; Indels 30; Gaps 6;

QY 243 ACAGCTCCACCAATCAACCCCAAGCTCTCCAAAAGATTATTAATGACCTCGGAGAA 302
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 Db 367 ACAGGTTCCAAACATCAATTAACAGTCAAAAGTCCAAAGTGTGCTTCTTCTGATGAGTA 426
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 QY 303 TATTTAATTCAGTGTGAAGCAAGGAAACCCGCCCAAGCTTTCTCGGACCCGTAA 362
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 Db 427 TTTTCAATTTGAATGTGAAGCTTAAGGAAATTCAGAACCAATTTTGTGTGACTTAAGA 486
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 QY 363 TGGACTCATTTTGAATGATTAAGACCTCTGTGTCAACATGAAGCTGTGACAGGAAC 422
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 Db 487 TGGCAACCTTTTATTTTCACTGACCATCGAGATTAATTCATGAACAAATTCAGAG- 541
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QY 423 GCTAATTAATCATCATGAGCGAAGGAAAGCTGAGACCTATGAGAGTCTATCAGTG 482
 DB 542 ----AATTTCAGATATCCCAACGAGGGGACATATCTCACTTTCAAGGAAATACCGCTG 597
 QY 483 TACAGCAAGAAAGAAAGCGGAGCTGCAGTTCTTAATTAACATTTGTTGCCGCCATCGAG 542
 DB 598 CTTTGCTTCAAAATTAACCTGGGATCCCTATGTGCAAGAAATGAAATTTATAGTTCCAG 657
 QY 543 ATCACCATTGTGGACCAAGAAAGAACTTGAACCAATCACACTTCAAGGGTCAGTCTT 602
 DB 658 TGTTCCAAACTCCCAAGAAAGAAATGACCTCTTGAAGTGGAGAGAGATCAAT 717
 QY 603 AGTACTTCCCTGAGACCCCAATTGATTAACCAACCTATATATTTTGTGATGATTA 662
 DB 718 TGTCCCTCCATGGAATCTTCCCAAGGCTCCCACTTTTACATTTATTTGATGAATAT 777
 QY 663 TTTCTTTCAAAAGCTTCCAAAGTGAAGATTTCTCAAGTTTGAATGGGACCTTTA 722
 DB 778 TGAATTAGAACACATGGAACAGATGAAAGATATCATGAGCCAAAGGAGATCTATA 837
 QY 723 TTTTTCCAATGTCTCCGAGAGACACCGCGAAGCTAATCTGTATGCTAGATTTAA 782
 DB 838 CTTTGGAAAGTGGAAAGAAAGGACAGTGGCAATGACTGTGCTTGTGCTGCAATTTCC 897
 QY 783 TCATACTCAACCATACAGAGAGAACCACTATTTCTGTGAAGGTGATTTCACTGATGA 842
 DB 898 AAGATTAGAGACTATTTGTACAGAAATGCAATGAATGAACGTTTAAAGCA 957
 QY 843 ATTGAATGACATTAAGCTGTCTAATTTGAGTGACCTGAGTTTATGTGCTTAATCAG 902
 DB 958 TGTATATGACTCAAGTTTCAACAGAAATTTGGTTCCAAAGGCAAAATTCATCAAGCAAG 1017
 QY 903 TTAGAGAGAGCCCAACCAATTTTAACTCCAGAAAGCAATGCAAGTAAACAAAGAGAA 962
 DB 1018 AAAACCCAACTGTCTGTGCTTCCACTGAGAGTGGAGTGTCTTAATTAACATCTCT 1077
 QY 963 AAGAGAGAAATGTGCTTTCACTGAGTGAATTTGCAAGAGAGCTGCTTACCCCAATTTTA 1022
 DB 1078 CAAGGGGAAATTTGCTGCTTGAAGTTTGTGCTGAAGCTTGCCAACTCCACAGTTGA 1137
 QY 1023 CTGGGCAAGAAAGATGAAATGCTACCCAAAAACAGACGTTTATTAAGACTTTGAGAA 1082
 DB 1138 TTGGAAACAAATTTGTGTGTGCTTACCAAAAGGGAGAGAAACAAAGAAATTTATGCA 1197
 QY 1083 AACCTGCAATATTCATGTTTCAAGAGAGACTGTGGAATTTACCAATGTATTAACAA 1142
 DB 1198 GACTTGAAGATGAGAAATGTCTTCCAGAGCAAAAGAAATTTATGCTGACACCCAG 1257
 QY 1143 AATGCAATTAGAGCCATCCATCACTATTTCTGTAGAGTTAAAGCGGCTTCATATCTG 1202
 DB 1258 CAATTTCTTGGGAACAGCCATCAGCATTTTCACTTATATGTAAGAGAGCTCTCGCTG 1317
 QY 1203 GATCAGAGCCCTCAAAATTTTGTGCTGTCCAGAGAGAGATGGAGCTTGTCTGAG 1262
 DB 1318 GACAAAGAAAGCTCAGAGTGTGTGTATGACCCGGAAGCAATGGCATCTTGTATGTGA 1377
 QY 1263 AGTATAGCAACCCCAACCCGAATTTGCTGTATTAACAAATGAGTCCCAATAGAAAT 1322
 DB 1378 GGTGTAAGGAACTTCAACCAATCAATGAGTGAAGTCAATGAGCTCCCGATTAACA 1437
 QY 1323 TGCCCTGATGACCCCAAGCAAGAAATAGATGGCGATACCATTAATTTTTCATATTTCA 1382
 DB 1438 TCAATCATTTG---CTGTGATGTGTCTTCCCAAGGAAATGATTTTATCAACTTCA 1494
 QY 1383 AGAAGATCAAGTGAAGTATATGATGCAATGCTCTTATGAATATGATATTTACTGGC 1442
 DB 1495 ACCAAATCAATCTGTGTGTATGACAGTGTGAAGCTCAAAATGTCCATGAACTATCTTCC 1554
 QY 1443 AAAAGCATTTGTAATGTGTGTGTGCTGAGCCACAGCAATCTCTACACCTGCAAAACACT 1502
 DB 1555 CAATGCAATATTTGATGT 1614
 QY 1503 CTACAGATCATGCAAAACAGGCTGTCTTACTAGACTGTGCTTCTTGGGTCTCTCTCT 1562

DB 1615 TTACCTACAGTGTGGGTACAGTCTTCTTCAATTTGCGAGTTCTTTGCTTCACTCGA 1674
 QY 1563 CCCAACATTCAGATGCTTTAAAGAGCTTAAAGAAAGTCTCTTCAATGAAATTTATGT 1622
 DB 1675 GGCAGTGTGTCTGTGCAAGAGTGAAGAGTGAACCCCTGGAGGCGAGCGGTATCA 1734
 QY 1623 TTTACATGAATATGAACTTTGGAATCAAGATGCTCATGAGATGTTTAAAGAAATTC 1682
 DB 1735 TATCTATGAATATGCAATTTGATGATCAACAGAACCCAGAAAGATGTGGTCTTGA 1794
 QY 1683 TGTGCCCCAAAGACAGTACAGAACTTATACGTGTGTGTGCAAGAAATTAATTTGGAT 1742
 DB 1795 CTATGTTGGGTGAAGAAATGCTATAGAAACCTGCACTGACAGCAATTTGATATTA 1854
 QY 1743 GGCAGAAATGAGTTCATTACAGCCCGAATATGCAATGTCGAAAGGAGCATGAT 1802
 DB 1855 AATGCTCAAAATCTTAAGATTTCTCTTAAGATCTGTATCCCAATTTGATATGCT 1914
 QY 1803 GTCTTTGATGCAAGTGAACATGATCACACTTATCCCTCACTGTCTGTGCTGTA 1862
 DB 1915 TGAATTTACTTGTGAAGCAATGTGACTCATTTGAAACACAGTTTGAAGTTGTCTCG 1974
 QY 1863 GGAACAAGGGAACTGCCAGATGAAGAGTTCACTGTGAACAAGATCATATGCT 1922
 DB 1975 GAGTAAAGTGAAGAGCTTTGA-----AATTAATGCAAGAAAGTGCAGAGAT 2025
 QY 1923 AGCTATGTCAGTACATGACAGAGGGGACCTTACAGTGTGTGCAACACACTCTGGA 1982
 DB 2026 AATTAATGATGAGCTAATTTGACCAATCTTAATGTAACCTTGAAGACCAAGTATTTA 2085
 QY 1983 CAGCTCTCCGCAAGCTGTGCTTAGAGTGTGCTCTCACTCCACTCCAGCTCCGT 2042
 DB 2086 CTGCTGTTTACGTCAATCTGCTCTTGAAGAGTGTCCGATA--TAACTCAAGTAACTGT 2142
 QY 2043 TTACATGTCCCAATTCCTCTCTTGACTTGAATCAATCACTTTGACAAAGTGT 2102
 DB 2143 TCTTATGTTCCGATTCACCAAGAAACCTTCACTGTCTGAAAGACAGAACAGATGT 2202
 QY 2103 TGAAGTTCATGAGACCCAGAGGATGACAACTAATGCCCCATTAACAAATCATATGA 2162
 DB 2203 TCGGCTGACCTGGGAAGCTGAGCTGACCAACAGCAATTTTACAGATATATTTTGA 2262
 QY 2163 ATATGAAGTGCATTAAGCAACAGCCAGGCTGTGACCAACCACTGAAGTTTCTGGAAC 2222
 DB 2263 ATTTGAAGGAACAAAGAAAGCTGGAAGTGGAGGAACGACAGGTCCAAAGAA 2322
 QY 2223 ACGACACAGCCCAAGCTGAGCTGTCTCTTACGTGAATCTCTCTTCCGCTGATGGC 2282
 DB 2323 GAAACCAACAGTATCTTACCTTTGCTCATTGTGATATCAAGTTCAAGGTCATATGC 2382
 QY 2283 AGTGAACAGCATTTGGAAGAGCTTCCAGAGGAGGCTGTGACGATTTTGAAGAAAGC 2342
 DB 2383 CGTGAACGAAGTAGGAAGATCAGCTTGAAGCGGTGACCACTATGAACACACACC 2442
 QY 2343 CTCAAGACAGATTAACAAACCCCAAGCTGTGGAAGAGCTGAGATGAGCTGATATTT 2402
 DB 2443 AGCAGCTCAGATAGGAATTCACAAACATTAAGGTTCAAGCTCTCAACCAAGGAAT 2502
 QY 2403 GGAAGATTAAGTGAAGCCCTTGAATGTTTGAATCTAATGGGCCAGGCTTCACTACA 2462
 DB 2503 GATTAATTAAGTGGAGCTTTTGAATTCATGAGAGATGAGCAAGGCTTGAAGTACAG 2562
 QY 2463 AGTTAGTGTGGCCGCAAGAAAGATGTGTGATGAATGACATCTGTGTGTGGCAAAATGT 2522
 DB 2563 AGTGAACCTGGAAGCAACAGGAGGCCAGTGAAGTGAAGAAAGAAAGATCAACAAAC 2621
 QY 2523 ATCCAAATATATTTCTGAGGACCCCACTTTTCTCATATCTGATCAAAAGTTCAGGC 2582
 DB 2622 --ACACATTTGGGGTGTGAGAGCCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2679
 QY 2583 CCGTAATGACATGGGTTTGGCCCGAGCCAGCTGTAGTCAATGGGACATTTCTGAGAAAG 2642

Db 2680 TATCATCACTAGAGCTGCGCTGACCCCTCAGTCACTCTATCTTGAGAGAGA 2739
QY 2643 CCTCCCAATGAGGCTCCTGGGAAGCGGTGTGAATGTGTAACAGTACCTTACCGA 2702
Db 2740 CTATCTGATACAGCTCCAGTGTCCATGCGGGGAGCGTTATTAACAGTACCTTATTA 2799
QY 2703 GGTGACCTGGAGCCAGTACCTCTGAAAAGCATCCAGAGACCTTCAAGGCTATCGAT 2762
Db 2800 AGTACCTGTGTCAAGCTTCCAAAGGACAGAGTACATGACGCTGAAAGGCTATCAGT 2859
QY 2763 TTAATCTGGAAGACCCAGAGTCTTAAAGAAACAGAGCTCATTGAGAAAAGT 2822
Db 2860 AAATGGTGGAAAACAAAAGTCTGTGATGGAAGAACATCCAAAAGAGTGAACAT 2919
QY 2823 CCTCACTTCCAGGAGAGACCTATGAGCAATGTTGCGGGCTGAGACCCCTTACCA 2882
Db 2920 TCTAAGATTTTCAGGACAAAAGAACTGTGAATGTTCTTCTTGAATGCTTGAAGTA 2979
QY 2883 CTACACACTGAATGTCCAGTGTCAATGGGAAGGGAGGCGCCAGCCCTGACAG 2942
Db 2980 ATTTCACTTAAAGCTTTGAGCCATTAATCTTAAAGAGCTGTGCTGAAAGTGAAGCTTA 3039
QY 2943 AGCTTTTAATCTCCAGAAAGAGTCCCAAGTGTCTCTGCTTGAAGATTGTGAATCC 3002
Db 3040 TATATTTCAAAACACGAAAGAGTACTGAACAGCAACTTTTCTAAAGTCACTAAAGT 3099
QY 3003 AACACGTGACTCTCTCACTTTGGAATGGATCCACGAGCCACCCGAATGGCATTTTGA 3062
Db 3100 TGATTAAGACACTGCGCACTTTTCTTGGGAGCTACTAAGAAATTAAGAAACTTAAC 3159
QY 3063 AGAGTACACTTAAGTATCAGCAATTAACAGACACATGAATGAGCCCTCTGTGTAGA 3122
Db 3160 TGGCTATCTTTGCAATATCAGTAAATTAATGACACTGACGATTTGAGAAATTAATGA 3219
QY 3123 TTGGAATTT---CTGCAACAGACACGCTGACTTTAAAAATTTAAATTTGACAC 3179
Db 3220 TATTAACATTAACATCCATCAAGGCCAGCTGACCTCTCAAACTGAAATGCACTAC 3279
QY 3180 TCGATTAAGTTTATTTCTATGACAAACATCAGAGATCAGAAAGTCAATTAACAA 3239
Db 3280 CAAGTAACAATTTCTACTTGAAGGCTTGCACTTCAAGGGCTGTGAAAACGATCAACGA 3339
QY 3240 GGAA 3243
Db 3340 GGAA 3343

RESULT 11
US-10-435-751-158
Sequence 158, Application US/10435751
Publication No. US20040053348A1
GENERAL INFORMATION:
APPLICANT: Agensys, Inc.
APPLICANT: Faries, Mary
APPLICANT: Challita-Bid, Pia M.
APPLICANT: Jakobovits, Aya
APPLICANT: Raitano, Arthur B.
APPLICANT: Ge, Wangmao
TITLE OF INVENTION: Nucleic Acids and Corresponding Proteins
FILE REFERENCE: 51158-20084.00
CURRENT APPLICATION NUMBER: US/10/435,751
PRIOR FILING DATE: 2003-05-09
PRIOR APPLICATION NUMBER: 60/404,306
PRIOR FILING DATE: 2002-08-16
PRIOR APPLICATION NUMBER: 60/423,290
PRIOR FILING DATE: 2002-11-01
NUMBER OF SEQ ID NOS: 208
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 158
LENGTH: 7650
TYPE: DNA
ORGANISM: Homo sapiens

US-10-435-751-158
Query Match 11.4%; Score 469.6; DB 13; Length 7650;
Best Local Similarity 48.8%; Pred. No. 1.1e-127;
Matches 1465; Conservative 0; Mismatches 1509; Indels 30; Gaps 6;

QY 243 ACAGCCTCCAAACCATACCCCAAGCTCTCAAAAGATTATTAATTAAGACCTCGGAGAA 302
Db 367 ACAGGTTCCAAACATTAATAAAGCTCAAAAGTCCAAAGTGGCTTTCCCTTGATGAGTA 426
QY 303 TATTTAATTCAGTGTGAAGCCAAAGGAAACCGCCCAAGCTTTCTCTGACCCGTAA 362
Db 427 TTTTCAAAATGATGTGAAGCTTAAAGAAATCCAAACCATTTTGTGTGATAGGA 486
QY 363 TGGGACTAATTTGATCAATGAAGCCCTGTGCTCAATGAAGCCGTGACAGAAAC 422
Db 487 TGGCAACCTTTTATTTTCACTGACCATGTGAATTCATGCAACATTCAGAA---- 541
QY 423 GCTCAATTAATTAATCATATGAGCGAAAGGAAAGCTGAGACTATGAAGAGTCTACGTG 482
Db 542 ----ACATTCAGGATCCCAAGAGGGGCAATATCTCACTTCAAGGAAATACCGCTG 597
QY 483 TACAGCAAGAAACGAACGCGAGCTGCAAGTTCTAATAACATTTGTTCGCCCATCCAG 542
Db 598 CTTTGCTTCAATATAAATCTGGGAATGCTATGTCAAGAAATAGAAATTTATAGTTCAG 657
QY 543 ATCAGCATTTGTGACCAAGAAAGAACTTGAACCATCACTCAAGTGTGACATCTTT 602
Db 658 TGTTCAAAACCTCCCAAGAAAGAAATTTGACCTCTTGAAGTGGAGGAGGATCCAT 717
QY 603 AGTACTCTCCCTGACAGACCCCAATTTGATTAACACCACTTAATATATTTTGGATGATTA 662
Db 718 TGTCTCCCATGATCATCTCCCAAGGCTCCCACTTACACATTTATGATGAATAT 777
QY 663 TTCTTTCAAGACTTCCAAAGTGAAGATTTCTAAGSTTTGAATGGGACCTTTA 722
Db 778 TGAATTAAGAACATCAAGAAAGAAAGTATATGATGACGCAAAAGGAGATCTATTA 837
QY 723 TTTTTCATATGCTCTCCAGAGGACACCCGGAACATATATCTTTATGCTAATTTAA 782
Db 838 CTTGCAACAGTGAAGAAAGGAGACATGCAATGCTGATCTGCTTGTGCTGCAATTTCC 897
QY 783 TCATACCTAAACCATACAGAGAAAGCACTATTTCTGTGAAGTGTATTCAGTGAATGA 842
Db 898 AAGATTAAGACATATGTAAGAAATGCAATGAATCTAACAGTTAAAGTAAGCA 957
QY 843 ATTTAATGACATATAGCTGCTAATTTGATGACACTAGTTTATGTGCTAAATCAAG 902
Db 958 TGTATATGACTCAAGTTCATCAAGAAATTTGCTTCAAGGCAATTCATCAACCAAG 1017
QY 903 TTAGAGAGGCGCAACATTTTAACTCCAGAAAGGCAATGCAAGTAAACAAAGAGAAAT 962
Db 1018 AAAACCCAAACCTGCTGTGCTCCCACTGAGAGTGGAGTGTCTTAATTAACATCT 1077
QY 963 AAGAGAAATGCTTTCATGAGTGAATGCAAGAGAGCTGCTTACCCCAATTAATTTA 1022
Db 1078 CAAGGGAAATCTTGTGCTGTGATGATGTTTGTCTGAAGCTTGCCTCAACAGTTGA 1137
QY 1023 CTGGCAAGAGAAATGATGCTAACCAAAACAGACAGTTTAAAGAACTTTGAGAA 1082
Db 1138 TTGAAACAAATTTGTGTGACTTTCACAAAGGGAGAGAAACAAAGAAATTAAGGCA 1197
QY 1083 AACCTTGACATGATTCATGTTTTCAGAGAGAGCTGTGAAATTAACATATGACAA 1142
Db 1198 GACTTGAAGATGAGATGCTCTTACAGAGACAAAGAAATTAATGCTGACAGCCAG 1257
QY 1143 AAATCATTTAGAGGCTATCCACATACATTTCTGTGATGATTAAGGCGCTCCTACTAG 1202
Db 1258 CAATTTCTTGGAGACAGCACTCAGATTTTACGTTTATATGAAAGAGCTCTCGCTG 1317
QY 1203 GATCAACGCTTCAAAATCTTGTGCTGTCCCAAGAGAGAGAGGAGCTTGTATGTGAG 1262
Db 1318 GACAAAGAGCTCAGAGTGTGTATAGACCGGAAGCAATGGCATCTTGTATGTGA 1377

QY 1263 AGCTAATGGCAACCCCAACCCAGATTAAGTGTGTTAACAATGAGAGTCCCAATAGAAAT 1322
 DB 1378 GGTGAGAGAGAACTCCAAACCCCAATCAAGTGAAGATCATGCTCCCACTGAGCA 1437
 QY 1323 TGCCTGTATGACCCGAGCAAGAAAATAGATGGCATACATTAATTTTCAATGTTCA 1382
 DB 1438 TCATCATTTG---CTGTGATGTGTCTCCCAAGGAAATCAGTTTACCAACCTTCA 1494
 QY 1383 AGAAGATCAAGTGCATATATCATGCAATGCTCTAATGAATATGATATTACTGGC 1442
 DB 1495 ACCAAATCAATGCTGTGTACAGTGAAGCTCAAAATGTCATGAGAACTATCTTTC 1554
 QY 1443 AAACGATTTGTAATGTGCTGGCTGAGCCACCAAGATCTTCAACCTGCAACACACT 1502
 DB 1555 CATGCAATATTAATGATGTGTGATGTCCGTCCATTTGATACAAACCAAGATGAGAAAA 1614
 QY 1503 CTACCAAGTCATTGCAAAAGGCTGCTTTTACTAGCTGTGCTTCTTGGGTCTCTCT 1562
 DB 1615 TTACGCTACAGTGTGGGTACAGTGTCTTCTTACATTCGAGTCTTGTCTTCACTGA 1674
 QY 1563 CCCAATCATGAGTGTGTTTAAAGAGACTAAAGAAATGCTCTTCAAGAAATATTATGT 1622
 DB 1675 GGCAGTGTCTCTGAGAGAGTGAAGAGAAACCCCTGAGAGGAGGAGGCTATCA 1734
 QY 1623 TTACATGAAAAATGAACTTTGGAATCAAGATGCTACATGATGCTTAAAGAAATTC 1682
 DB 1735 TATCTATGAAAAATGCAATGCAATGCAATCAAGAACACCAAGAAAGATGCTGGCTTA 1794
 QY 1683 TGTGCCCCAAAGAGACATGACAGAACTTATACGTGTGTTCAGAGAAATTAATGAGAT 1742
 DB 1795 CTATGTTGGGTGAAAAATGCTATAGAAAAATCTGACATCACAGCAATTTGGATTAATG 1854
 QY 1743 GCGAAAGATGAAATGCTTACCTTACGCCAATATGAGTTGCAAGAGGAGAGCATGTGT 1802
 DB 1855 AAATGCTCAAAAATTAGATTTCTCTTAAGAAATCTCGATCCCAATTTGCAATGCT 1914
 QY 1803 GTCTTTGATGCAAGATGAAATCATGATCAACCTTATCCCTCACTGCTGTGCTGCA 1862
 DB 1915 TGAATTAATGATGAAAGCAAAATGTGATCAATTTGAAACAGATTTGAATGTCTCG 1974
 QY 1863 GGAACAACAGGAACTGCCCCAGTATGAAAGTTCACTGTTGACAGAGATCACTATGTGT 1922
 DB 1975 GAGTAAGATGAGAGAGCTTTGA-----AATTAATGACAGAGATGAGAGAT 2025
 QY 1923 AGTGAATGTCAGTGAAGTGAACAGCGGAGCTTACAGTGTGTGCCAACACACTGTGA 1982
 DB 2026 AATTATTTGATGAGCTAATTTTGAACATATCTAATGTAATCTTTAGAGACCAAGTATTTA 2085
 QY 1983 CAGCGTCTCCGAGGCTGTGTGCTTACGCTTGTGCTCTCACTCAACTCCAGCTCCGT 2042
 DB 2086 CTGCTGTTCACTCACTGCTCTTACAGATGCTGTCGATTA---TAACTCAATATCTGT 2142
 QY 2043 TTAAGATGCTCAAAATCTCTCTTTTGAATGAATGACATCAACTTGAACAAAGTGT 2102
 DB 2143 TCTTATGTTTCCGAGTCCACAGAAAACTTCACTTGTGAAAGACAGAAACGAGGTGT 2202
 QY 2103 TCGCTGATGAGACCCGAGGAGTGAACAACATATGCCCATTAACAAATTAATCATCTGA 2162
 DB 2203 TCGGCTGACCTGGAGAGCTGAGACTGACACACAGAAATATTAGAGAGATATGTGTGA 2262
 QY 2163 ATATGAAGATGCAATGACACAAAGCAGGAGCTGTGACACACAAATGAAATTTTGGAAAC 2222
 DB 2263 ATTTGAAGAGAAACAAAGAGAGCTGGAAGTGGAGAGAACTGACAGAGTCCAGAGAAA 2322
 QY 2223 ACAGACCAAGCCCACTGAAGCTGTCTCTTAAGTAACTACTCTTCCGCTGATGAGC 2282
 DB 2323 GAAAAACACAGTATCTTACTTTGGCTCATTTTGAAGATACAGTTCAGGGTCTATAC 2382
 QY 2283 AGTGAACAGATTTGGAGAGAGCTTGGCCAGCGAGGCTGTGAGACATTTTGAAGAAAC 2342
 DB 2383 CGTGAACGAAGTGAAGAGAGTCAAGCTTACAGCGGTGACAGCAATCATGAAACACACACC 2442

QY 2343 CTCAGAACAGATTAATAAACCCCAAGCTGTGGAAGAGACTGGAGATCAGCTGATTAATTT 2402
 DB 2443 AGCAGCTCAAGATAGAAATTCACAAACATAAAGGTTCAAGCTCTCAACCCAGAGAAAT 2502
 QY 2403 GGAAGTTACGTGAAGAGCTTGAATGTGTTGAAATCTTAATGGGCCAGGCTTCAATACAA 2462
 DB 2503 GATTAATAAGTGGAGCTTTGAAATTCATGAGAGAGATGAGACAGGCTTGAAGTACAG 2562
 QY 2463 AGTTAGTGGCGCAGAAAGATGTGATGATGAATGACATCTGTGTGTTGGCAAAATGT 2522
 DB 2563 AGTGAATCTGAAGAACCAAGAGAGCCCAAGTGAAGTGGAGAGAGAAAGAAAGTACAAAC 2621
 QY 2523 ATCAAAATATATGTCTAGAGCAAGCAACCTTTGTTCATATCTGATCAAAAGTTGAGC 2582
 DB 2622 --ACAAATGTGGAGATGAGACGCTGTGTATCTGCTTATGATGATCAAGTCCAGGC 2679
 QY 2583 CCTGAATGACATGGGAGTTTGGCCCGGAGCCAGCTGTATGATGAGCAATTCGAGAGAA 2642
 DB 2680 TATCAATCAATGAGATCTGGGCTGAGCCCTGACCTGATGATGATCTTATCTGAGAGAA 2739
 QY 2643 CCTCCCAATGTGTGCTCTGGGAAAGTGCATGTGATGTGTAACAGTACTTGAACCGA 2702
 DB 2740 CTATCTGATACAGCTCCAGTATCATGAGGAGTGAAGCTTATTAACAGATCAATTAATGA 2799
 QY 2703 GGTGACATGGAGCCAGTACTCTGAAGAGATCCGAGAGACCTTCAAGGCTATGAGAT 2762
 DB 2800 AGTTACTGTGTCAACAGTCTTCAAGAGACAGTACATGAGACGCTGAAAGGCTATCAGAT 2859
 QY 2763 TTACTATTTGAAGAGACCCAGAGTTCATTAAGAAACAGAGCTCATTTGAGAAAGAT 2822
 DB 2860 AAATGTGAGAAACAAAGAGCTGTGTGATGAGAAACACATCCCAAGAGATGACAT 2919
 QY 2823 CCTCACTTCCAAAGCAGCAAGACTCATGAGCATGTGCTGGGAGCTTGAAGCCCTTGAACA 2882
 DB 2920 TCTAAGATTTTGAAGAGAAAGAACTGAGATGATGTTCTTCTTAAGATGCTTTAATGA 2979
 QY 2883 CTACACACTGAATGTCCAGTGTGCAATGAGAAAGGAGGAGCCCAAGCCTGACAG 2942
 DB 2980 AATTCAATTAACAGTCTTGAAGCTTATTAACCTTAAAGAGCTGTGCTGAAAGTGAACCTTA 3039
 QY 2943 AGCTTTTAATTAATCCAGAAAGAGTCCCAAGTCTCCCTGTCTTGAAGATTTGAATCC 3002
 DB 3040 TATATTTCAACACAGAGAGAGTACTGAACAGCACTTTCTTAAGATCATCAAGT 3099
 QY 3003 AACACTGACCTCTCACTTTGGAATGGATTCACCGAGCCACCCGAATGCAATTTTGAAC 3062
 DB 3100 TGAATAAGACATGCACTTATCTTGGGAGCTTACTTAAGAAATTAATGAAACTTAAC 3159
 QY 3063 AGAGTACACTTAAAGTATCAGCCAAATTAACGACACATGAATTAAGGCTCTGTGAGA 3122
 DB 3160 TGGCTATCTTTTGAATATCAATATTAATGAACACTTACGAGATTTGGAGAAATTAATGA 3219
 QY 3123 TTTGAAATTT---CTGCAACAAAGACAGGAGCTTTAAATAATTAATTTAGAGC 3179
 DB 3220 TATTAACATTAACATCTCAATCAAGCCAGCTGAGCCTCTCAACCTGAATGCACTAC 3279
 QY 3180 TCGATATAAGTTTATTTCTATGACAAACATCAAGAGATCAGAGATCAATTAACGA 3239
 DB 3280 CAAGTACAAATTTCTACTTGAAGGCTTGAACCTTCAAGGCTGTGAGAAACGATCAACGA 3339
 QY 3240 GGAA 3243
 DB 3340 GGAA 3343

RESULT 12
 US-10-435-751-164
 ; Sequence 164, Application US/10435751
 ; Publication No. US20040053348A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Agensys, Inc.
 ; APPLICANT: Farris, Mary
 ; APPLICANT: Chailite-Bid, Pia M.

APPLICANT: Jakobovits, Aya
APPLICANT: Raitano, Arthur B.
APPLICANT: Ge, Wangmao
TITLE OF INVENTION: Nucleic Acids and Corresponding Proteins
FILE REFERENCE: 51158-20084.00
CURRENT APPLICATION NUMBER: US/10/435,751
CURRENT FILING DATE: 2003-05-09
PRIORITY APPLICATION NUMBER: 60/404,306
PRIORITY FILING DATE: 2002-08-16
PRIORITY APPLICATION NUMBER: 60/423,290
PRIORITY FILING DATE: 2002-11-01
NUMBER OF SEQ ID NOS: 208
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 164
LENGTH: 7650
TYPE: DNA
ORGANISM: Homo sapiens
US-10-435-751-164

Query Match 11.4%; Score 469.6; DB 13; Length 7650;
Best Local Similarity 48.8%; Pred. No. 1.1e-127;
Matches 1465; Conservative 0; Mismatches 1509; Indels 30; Gaps 6;

243 ACAGCCTCCACCATCACCACCAAGTCTCCAAAGATTACATTATTGACCTCGGAGAA 302
367 ACAGGTTCCACCATCATATAAAGTCAAAAGTCCAAAGTGGCTTCCCTTGATGATGA 426
303 TATTTGATTCAGTGTGAAGCCAAAGGAAACCGCCCGCCAGCTTTCTGAGCCGTA 362
427 TTTTCAATATGATGAGGCTAAAGGAATCCAGAACCAATTTTCTGATCAAGA 486
363 TGGGACTATTTTGATCATGATTAAGACCTCTGTCGACATGAAAGCTCGACAGAAC 422
487 TGGCAACCTTTTATTTATCTGACCATGATGATTAATTCATGACAAATTCAGA---- 541
423 GCTCAATTAATCATCATGAGGAGAAAGCTGAGACCTATGAAAGAGTCTATCAGT 482
542 ----ACATTGAGATCCCAAGAGGAGGACATATCTCATTTCAGAGGAATACCGCTG 597
483 TACAGCAAGAAAGAAACCGGAGCTGCACTTTCTAATAACATTTGTCGCGCCATCCAG 542
598 CTTTGCTTCAATAAATGAGGATGCTATGTCAGAAAGATTAATTAATGTTCCAG 657
543 ATCACCATTGTGACCAAGAAAGAACTTGAACCATCAGCTTCAAGTGTCACTTT 602
658 TGTTCCTCAAACTCCCAAGAAAGAAATTAACCTCTTGAAGTGAAGAGGAGATCCAT 717
603 AGTACTCTCCGAGAGCCCAATTGATTAACACCACTATTAATTTTGGATGGATGA 662
718 TGTCTCTCCATGATCTCCCAAGAGCTCCCACTTTTACATTTATTTAGATGAATAT 777
663 TTTCTTTCAAGACTTCCCAAGAGAGAGTTCCTCAAGTGTGATGAGGAGCTTTA 722
778 TGAATTTAGAACATGAGAACAGATGAAGATATCATGAGCAAAAGAGAGATCTATA 837
723 TTTTTCATATGTCCTCCAGAGACACCGCGAAGATATATCTGTTATGCTAGATTAA 782
838 CTTTGGAAACGTGAGAAAGAGACAGTGCATGACTCTGTGCTTTGCTGCAATTTCC 897
783 TCATATCTCAACCATACAGCAGAGCACTTATTTCTGAGAGGATTTCAAGTGATGA 842
898 AAGATTAGGACTATTTGTAAGAAATGCAATGAAATTAACATGATTAAGCA 957
843 ATTGATGACACTATAGCTGCTAATTTGAGTCACTGATTTTATGCTGCTAAATCAG 902
958 TGTATATGACTCAAGTTATTCACAGAAATGTTTCAGAGCAAAATTCATCAGAGAA 1017
903 TTAGAGAGGCCCAACCAATTTTAACTCAGAAAGCAATGCAAGTAACAAAGAGAAAT 962
1018 AAAACCCCAACTGCTGTGCTCCCTCCAGAGAGTGCAGTGTCTTCAATTAACATCT 1077
963 AAGAGAAATGTGCTTCACTGAGAGTGCATGACAGAAAGCTGCTACCCCAATTAATTA 1022

1078 CAAGGGGAAATCTGTGCTTGAAGTGTGCTGAAAGGCTTGGCCAACTCCACAGCTTGA 1137
1023 CTGGCCAAAGAAATGTAATGCTACCAAAACAGACATTTATAGACTTTGAGAA 1082
1138 TTGGAACAAATTTGTGTGACTTACAAAGGGAGAGAAACAAAGAAATTTATGCGAA 1197
1083 AACCTGAGATCATTCATGTTTTCAGAGACAGACTCTGAATTAACATGATATGACAA 1142
1198 GACTTTGAAGATAGAAATGCTCTCTACAGAGCAAAAGAAATTTATCTCTCAGAGCAG 1257
1143 AAATCATTTAGAGCATTCACCATCATTTCTGTAGTTAAAGGCTCTCATCTG 1202
1258 CAATTTCTTGGAAAGCAGCACTCAGATTTTCAAGTTATAGAGAGAGCTCTCGCTG 1317
1203 GATCAGACCTCTCAAAATCTTGTGCTCTCCAGAGAGAGATGAGACCTTATGCGAG 1262
1318 GACAAAGAGCTCTCAGATGCTGTGTATAGACCGGAAGCAATGCGATCTGTATATGTA 1377
1263 AGCTAATGCAACCCCAACCGAATTAAGCTGTGTTAACTAATGAGTCCCAATGAAAT 1322
1378 GCTGAAAGAGACTTCAACCAATCAATAGTGAAGTCAATGCTCCCAAGTTGACAA 1437
1323 TGCCCTGATGACCCAGCAGAGAAATGATGCGATACCATTTATTTTCAATGTTCA 1382
1438 TCATCATTTG---CTGTGATGTTGCTTCCAGAGAAATCAGTTTACCAACTTCA 1494
1383 AGAAATGCAAGTGAATATCATGTCATGCTCTTAATGATATGATATTTATCTGCG 1442
1495 ACCAATATATCTGCTGTGATCAGATGAGAGCTCAATATGCAATGCAATCTATCTTGC 1554
1443 AAAGCATTTGAAATGCTGCTGAGCAGCAGCAACGAATCTCACACCTGCAACACT 1502
1555 CAATCCAAATTTGATGTTGATGATGCTGCTCTCAATGATTAACAAAGATGAGAAA 1614
1503 CTACAGGTCAATTCGAAACAGGCTCTTTAATGATCTGTCCTTTTGGGCTCTCT 1562
1615 TTAGCTACAGTGTGAGTGAAGTCTTCTTACATTTGAGGATCTTTTGGCTTCACTGA 1674
1563 CCCAATCATGAGTGTGTTAAAGAGCTAAAGAAAGTCTCTTCAAGAAATTTATGAT 1622
1675 GGCAGTCTGTCTGCGCAGAAAGTGAAGAAAGTGAACCCCTGAGGCGAGCGGTATCA 1734
1623 TTTTATGAAATGGAATTTTGAATTAAGATGCTATGATGCTTAAAGAAATCC 1682
1735 TATCTATAAATGCAATTCAGATGATCAAGAAACCAAGAAAGATGCTGCTTTA 1794
1683 TGTGCCCCAAAGCAGTACAGAACTTATACGTGTGTCAGAGAAATTAATGAGAT 1742
1795 CTGATGTTGGTGAAGAAATGCTATAGAGAAACAGTCAAGCCATTTGATATTAAG 1854
1743 GGCAGAAATGAAGTTCATTAAGCCGCAATATGCACTGTGCAAGAGAGATGCT 1802
1855 AAATCTCAAAACTTAAGATTTCTCTTAAGAAATCTGTATCCCAATATGCAATCT 1914
1803 GTTCTTGAATGCAAGGAAATGATACACCTTATCCCTCATCTGCTGTGCTGAA 1862
1915 TGAATTAATGTAAGCAAAATGACTCATATTGAACACAGTTGAAGTGTCTG 1974
1863 GGAACAAGAGAACTGCGCAGTGAATGAAGTTCATCTTTGACAGATCATCTAGTGT 1922
1975 GAGTAAATAGAGAGAGCTTTGA-----AATTAATGCAACAGAAATGAGAGAT 2025
1923 AGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1982
2026 AATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2085
1983 CAGGCTCTCCGCGAGGCTGTGCTTGAAGTGTGCTCTCAATCTCAGCTCCGCT 2042
2086 CTGCTTCACTCACTGCTCTGATGATGATGATGATGATGATGATGATGATGATGAT 2142
2043 TTACATGCTCCCAATCTCTCTTGAATTTGAATGATGATGATGATGATGATGATGAT 2102

Db	2143	TCTTGATGTTCCGGATTCACACGAAAACCTTCACTTGTCTGAAGAAGACGAAACAGAGTGT	2202
Qy	2103	TCAGCTGTCATGAGACCCCAAGCGATGACAACTATAGCCCTTATCAAAATTCATCATCGA	2162
Db	2203	TCGGCTGACCTGGGAAGCTGGAGCTGACCAACACAGCAATATTATGCGATTTATATGTTTGA	2262
Qy	2163	ATTATGAATGCAATGACCAAGCCAGGGCTGGGACCAACCAACTGAAGTTTCCGAC	2222
Db	2263	ATTGAAAGAAAACAAAGAAGACCTGGAAAGTGGAGAACTGACAGAGTCCAAAGGAA	2322
Qy	2223	ACAGACCAAGCCCAAGCTGAAAGCTGTCTCTTACGTGAACCTACTCTTCCGCGTATGGC	2282
Db	2323	GAAAACCAAGTATCTTACCTTTGGCTGCATTTGTGAGATTCACAGTTCAAGGTCATATGC	2382
Qy	2283	AGTGAACGCAATTGGGAAGAGCTTGCCAGCGAGCGCTGTGAGCATTTTGACGAAAGC	2342
Db	2383	CGTGAAACGAAGTAAAGGAAAGTCAGCCTTAGCGACGCGTCAACATCATGAAACCAACC	2442
Qy	2343	CTCGAACCAAGTAAAAACCCACAGCTGTGGAAAGGACTGGGATTCAGAGCCGTGAATTT	2402
Db	2443	AGCAGCTCCAGATAGGAATCCACAAACATTAAGGTTCAAGCTTCAACCCAAAGAAAT	2502
Qy	2403	GGAAGTATACGTGAAGCCCTTGAATGTGTTGCAATCTATAGGCGCAGGCTTTCAGTACA	2462
Db	2503	GATTTATTAAGTGGAGCCTTTGAAATTCATGAGACAGATATGACCAAGCCTTAGATCAG	2562
Qy	2463	AGTTAGCTGGCGCCAGAAAAGATGTGATGATGAATGCAATCTGTGGTTGTGGCAATGT	2522
Db	2563	AGTGACCTGGAAAGCCACAGGGAGCCCAAGTGAAGTGGAAAGAAACAGTCACAAACC-	2621
Qy	2523	ATCCAAATATATTGTCTGACGACCGCCAACTTTTGTTCATATCCGATCANAAGTTCCAGC	2582
Db	2622	--ACCAATGGGGGATGAGCGCTGTCTATAGCCCTTATATGATGATCAAGTCCAGGC	2679
Qy	2583	CCTGAATGACATGGGGTTTGGCCCCCGAGCCACAGCTGTATCATATGGGCACTTCTGAGAAGA	2642
Db	2680	TATCATATCAATAGATCTGGGCGCTGACCTTCAGCATGATCTCTATTTCTGAGAAGA	2739
Qy	2643	CCTCCCAATGCTGCTCCTGGGAACGTGCGTGTGATGTGTGAAACAGTACTTACCCGA	2702
Db	2740	CTATCTGTATACAGCTCCAGTGATCATATGGGGTGAAGCTTATTAACAGTATCATTTAA	2799
Qy	2703	GGTGACCTGGGACCCAGTATCTTGAAGAAAGCATCCGAGAACACTTACAAAGCTATCGAT	2762
Db	2800	AGTTACCTGGTCMACAGTTCCAAAGGACAGGTATGATGACGTCGAAAGGCTATCAAT	2859
Qy	2763	TTACTATTGGAAGACCCAGAGTTCACTTAAAGAAACAGCGTCACTTGAAGAAAAGAT	2822
Db	2860	AAATTGGTGAAGAAACAAAAGTCTTGGATGGAAGAACATCCCAAGAAAGTGAAT	2919
Qy	2823	CCTCACTTCCAAAGGACAGACATCATGGCATGTGTGCGGGGCTAGAGCCCTTATGCCA	2882
Db	2920	TCTAAGATTTTCAAGACAAAGAAACTGTGAATGTTCTTCTTAAAGTCTTTAATGA	2979
Qy	2883	CTACACACTGAATGTCCAGTGTGTCATATGGGAAGGGAGGGCCAGCGACCTTGACAG	2942
Db	2980	ATTTCATTTAACAGCTTAAAGCTTATATACCTTAAAGAGACCTGGTCTCTGAAGTGAACCTTA	3039
Qy	2943	AGCTTTTAATCTCCAGAAAGAGTCCCAAGTGCCTCCGTCTTGAAGATTTGAATCC	3002
Db	3040	TATATTTCAAAACCAAGAAAGGATACCTGAAACAGCAACTTTCTAAAGTGCATCAAGT	3099
Qy	3003	AACACTGAGCTCTCTCACTTTGGAATGGGATTCACCGAGCAACCCGAATGGCATTTTGAAC	3062
Db	3100	TGATTAAGACACTGCCATTTTATCTTGGGACCTACCTTAAGAAATTAATATGAAACTTAAC	3159
Qy	3063	AGAGTACACTTAAAGTATGAGCAATTAACGACACATGATTAATGGCCCTCTGTGTAGA	3122
Db	3160	TGGCTATCTTTTGCATATCATGATTAATTAATGACACCTTACGAGATTTGAGATTAATATGA	3219
Qy	3123	TTTGAATTT---CCTGCCAACAAACACGCTGAGCTTTAAAAAATTTAAATTTTCAGAC	3179
Db	3220	TATTAACATTAACACTTCATCAAGCCCAAGCTGGGACCTTCAAACTGAATGCAATAC	3279

QY	3180	TCGATATAGTTTATTTCTATGACAAACATCGACGAGATCAGAACTCAATATACAGA	323
Db	3280	CAGATACAAATTTCTATTGAGGGCTTGACATTCACAGGGCTGTGAAACCAGATCACGGA	333
QY	3240	CGAA 3243	
Db	3340	CGAA 3343	

RESULT 13

US-10-435-751-170

; Sequence 170; Application US/10435751

; Publication No. US20040053348A1

GENERAL INFORMATION:

; APPLICANT: Agensys, Inc.

; APPLICANT: Paris, Mary

; APPLICANT: Chailitea-Bid, Pia M.

; APPLICANT: Jakobovits, Aya

; APPLICANT: Raitano, Arthur B.

; APPLICANT: Ge, Wangmao

; TITLE OF INVENTION: Nucleic Acids and Corresponding Proteins

; TITLE OF INVENTION: Entitled 282PIG3 Useful in Treatment and Detection of C

; FILE REFERENCE: 51158-20084.00

; CURRENT APPLICATION NUMBER: US/10/435,751

; CURRENT FILING DATE: 2003-05-09

; PRIOR APPLICATION NUMBER: 60/404,306

; PRIOR FILING DATE: 2002-08-16

; PRIOR APPLICATION NUMBER: 60/423,290

; PRIOR FILING DATE: 2002-11-01

; NUMBER OF SEQ ID NOS: 208

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 170

; LENGTH: 7650

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-435-751-170

QY	243	ACAGCTCCACACCATCAACCCAAAGTCCTCCAAAAGATTACATTAATGACCTCCGGAGAA	302
Db	367	ACAGGTCACAAATCATATAAAGTCACAAAGTCCAAAGTGCCTTCCCTTCGATGAGTA	426
QY	303	TATTGATTCAGTGTGAAGCCAAAGGAAACCCGCCCAAGCTTTCTCGAACCCCTTA	362
Db	427	TTTTCAAATGAAATGTGAAGCTAAAGAAATCCAGAACCAATTTTGTGTGACTAAGGA	486
QY	363	TGGAGCTCATTTTGACATGATGATTAAGACCTCTGTGTCAACATGAAGCTGCGACAGAAC	422
Db	487	TGGCAACCTTTTATTTTCACTGACATCGGATTAATTCATCGAACAATTCAGGA-----	541
QY	423	GCTCATATTTAACTCATGAGCGAAAGGAAAGCTGAGACCTATGAGAAGATCTATCAGTG	482
Db	542	-----ACATTCCAGATCCCAAAAGGGGACACATATCTGACCTTTCAGGAAATATCCGCTG	597
QY	483	TACAGCAAGAAAGAAACGCGAGCTGCAGTTTCTTAATAACATTTGTCGCCCATCCAG	542
Db	598	CTTGCTCTCAATTAATATCGGAATCGCTATGTCAAGAAATTAATTAATTTAGTTCCAAAG	657
QY	543	ATCACCAATTTGAGACCAAGAAAACTTGAACCAATCACTTCAAAATGCTGACTCTTT	602
Db	658	TGTTCCAAACCTCCCAAAAGAAAAATTTGACCCCTTGAAGTGAAGAGGAGATCCAAAT	717
QY	603	AGTACTTCCCTGACAGACCCCAATTTGATTAACACCACTTAATATTTTGGATGGATTA	662
Db	718	TGTCTCTCCATGACATCTTCCCAAAAGGCTCCCACTTTTACATATTTATGGATGAATAT	777
QY	663	TTCCCTTCAAAAGCTTCCAAAGAAAGTGAAGAGTTTCTCAAGTTTGAATGGGAGCCTTTA	722
Db	778	TGAATTTAGAACATCGAACCAAGATGAAGAGTATACATGAGCCAAAAAGGAGATCTTATA	837

QY 723 TTTTCCATGTCCTCCAGAGACACCCGGAAGCTATATCTGTATCTAGATTAA 782
DB 838 CTTGGAAGCTGGAAGAAAGAGACAGTGCATGACTGTGCTTGTCTGATTTCC 897
QY 783 TCACTACTCAACCAATACAGAGAAAGCACTATTTCTGTGAGGTGATTTCACTGATGA 842
DB 898 AAGATTAAAGCACTATTGTACAGAAATGCCAAATGAACTTAACAGTTTAAAGCA 957
QY 843 ATTGAATGACATATAGCTGTAAATTGAGTACATGAGATTTTATGCTGTAAATCAAG 902
DB 958 TGTCTAATGACTCAAGTTTCAATCCAGAAATTTGTTCCAAAGCAAAATTCATCAAGCAAG 1017
QY 903 TTAGAGAGGCGCCAAACATTTTAACTCCAGAAAGCAATGCAAGTAAACAAGAGAAAT 962
DB 1018 AAAACCCAAATCTGTGTGCTCCCACTGAGAGTGGAGTCTTCAATTAACATCTCT 1077
QY 963 AAGAGAAATGTGCTTCTCACTGAGTGTGATGCAAGAGACATGCTTACCCCAATTAATTA 1022
DB 1078 CAAGGGGAAATCTGTGCTGTGAGTGTGCTTGAAGGCTTCCAACTCCACAGGTGA 1137
QY 1023 CTGGGCAAGAGATGAGATGCTACCCAAAACAGACAGTTTATTAAGAACTTTAGAA 1082
DB 1138 TTGGAACAAATTTGTGTGACTTACCAAGGGGAGAGAAACAAAAGAAATTTATGCA 1197
QY 1083 AACCTGCAGATCATTCATGTTTCAAGAGCACTGGAATTTACCAATGTATAGCAAA 1142
DB 1198 GACTTGAAGATGAGAAATGTCTCTACAGAGCAAAAGAAATTTATGCTGACAGCCAG 1257
QY 1143 AAATGATTAGAGCAATCCATACCATTTCTGTAGAGTTAAAGCGGCTCATATCTG 1202
DB 1258 CAATTTCTGGGAACAGCCACTCACGATTTTCACTTATAGTAAGAGGCTCTCGCTG 1317
QY 1203 GATCAGAGCCCTCAAAATCTTGTGCTGTCTCCAGAGAGAGATGGAACCTTATCTGAG 1262
DB 1318 GACAAAGAAAGCTCAAGAGTGTGTATAGCACCGAGAGCAATGGAATCTTGTATGTGA 1377
QY 1263 AGCTAATGGAACCCCAACCCAGAAATTTAGCTGTTAACTAATGAGTCCCAATAGAAAT 1322
DB 1378 GGTGTAAGAGAACTTCAACCCCAATCAATGAGAGATCAATGAGCTCCCACTTGAACA 1437
QY 1323 TGGCCCTGATGACCCGAGCAAGAAATAGATGCGATACCATTTATTTTCAATGTTGA 1382
DB 1438 TATATCATTTG---CTGTGATGTGTCTTCCCAAGGAAATAGTTTTACCACTTGA 1494
QY 1383 AGAAGATCAAGTGCATATATAGTCAATGCTCTTAATGAATATGATATTTACTGCG 1442
DB 1495 ACCAATCATACTGCTGTGTACAGAGTGAAGCTCAAAATGTCATGAGAACTATCCCTGC 1554
QY 1443 AAGCAATTTGTAATGTGTGCTGAGCAACCAAGAACTCTACACCTGCAAAACACT 1502
DB 1555 CAATGCAATATTTAGATGTGTGAGATGTCCGTCCATTTGATACAAACCAAGATGAGAAAA 1614
QY 1503 CTACAGATCATTTGCAACAGGCTGCTTTACTAGATGCTGCTTGTGGTCTGCTCT 1562
DB 1615 TTACGCTACAGGTGTGGGTAGAGTCTTTCTTAATGAGATTTGCTTCACTTGA 1674
QY 1563 CCCAACCATGAGTGTTTAAAGAGCTAAAGAGTGTCTTTCATGAAGATTTATGT 1622
DB 1675 GGCAGTGTGTCTGCAAGAGGTGAGAAAGTAAACCTGGAAGGCGAGGATATA 1734
QY 1623 TTTTACATGAATGAATCTTTGAAATCAAAAGATGCTATAGATGCTTAAAGAAATTC 1682
DB 1735 TATCTATGAAATGTGCAATGCAATCAACAGAACACCGAAAGATGCTGGCTTA 1794
QY 1683 TGTGGCCCAAGAGACATGACAGAACTTATACGTGTGTGCAAGAGATTAATTAAGGAT 1742
DB 1795 CTCATGTGGTGAAGAAATGCTATAGAAATCTGAGTCAAGCCAAATTTGGATATTAAG 1854
QY 1743 GGCAGAAATGAATTTCACTTACAGCCGAATATGCAATTTGCAAGAGGAGATGCT 1802
DB 1855 AAATGCTACAAACTTGAAGTGTCTCTTAAGAAATCTCTGATCTCCCAATTTGATATGCT 1914

QY 1803 GTTCTTGAATGCAAGTGAACAAATGATACACCTTATCCCTCACTGTCTGTGCTGA 1862
DB 1915 TGAATTAATTTGAAAGAAATGTGACTCAATTTGAAACACAGTTTGAAGTTGTCTG 1974
QY 1863 GGAACAAGAGAACTGCCCAGATGATGAAGTTCACTGTTGACAGAGATCATTAAGTGT 1922
DB 1975 GAGTAAAGATGAGAAAGCTTTTGA-----AATTAATGACAGAAAGATGAGAGAT 2025
QY 1923 AGCTGATGCAATGACATGACAGGCGGACCTTACAGTGTGTGAGCCCAACACTGTGA 1982
DB 2026 AATTAATTAATGAGTAAATTTGACATATCTAATGTAACTTTAGAGACCAAGATTTTA 2085
QY 1983 CAGGCTCTCCGAGCGCTGTGCTTAAAGCTGTGTGCTTCACTCACTCACTGCTCCGT 2042
DB 2086 CTGCTGTGAGTCAATCTGCTCTTGAAGAGTGTGCGAT---TAACTCAAGTAACTGT 2142
QY 2043 TTAAGATGCCAAATCTCTCTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 2102
DB 2143 TCTTGAATGTTCCGATCCACAGAAACCTTCACTGTCTGAAGACAGAAAGAGTGT 2202
QY 2103 TGAGCTGTGATGACCCCGAGGAGTGAACAATAGCCCAATTAACAAATTCATCATGA 2162
DB 2203 TGGCTGACCTGGAGAGCTGAGCTGACCAACAGCAATTTAGAGATATTTGTGA 2262
QY 2163 ATATGAAGATGCAATGACCAACAGGCGTGTGCAACCAACATGAAGTTTCTGGAAC 2222
DB 2263 AATTGAAGAAACAAAGAAAGCTGTGAAGTGTGGAAGAACTGACAGATCTCAAGAAA 2322
QY 2223 ACAGACCAAGCCAGCTGAGCTGTCTTCTTACGTGAATCTATCTCTTCCGCTGTATGC 2282
DB 2323 GAAACCAAGATATCTTCACTTTGCTCATTGTGTGATATCAAGTTCAAGGCTCATAGC 2382
QY 2283 AGTGAACAGCATTTGGAAGAGCTTCCAGCAAGCGCTGTGAGATATTTAGCAAAAC 2342
DB 2383 CGTGAACGAAGTGAAGAGATGACCTTGAAGCGCTGACATCAATGAAGAAACACAC 2442
QY 2343 CTCAAGACCAATTAACAAACCCCAAGCTGTGAAGAACTGGATGAGAGCTGTATATTT 2402
DB 2443 AGCAGCTCAAGTATGAAATTCACAAACATTAAGGTTCAAGCTTCAACCCAAAGAAAT 2502
QY 2403 GGAAGATTAAGTGAAGCCCTTGAATGTGTTGAAATCTAATGAGCAAGGCTTCAATCA 2462
DB 2503 GATTAATTAAGTGAAGCTTGTAAATCCATGAGCAAGATGAGCAAGGCTTGAATGAC 2562
QY 2463 AGTACCTGAGCCCAAGAAAGATGTGATGATGAATGACATCTGTGTGTGCAAAATGT 2522
DB 2563 AGTGAACCTGGAAGCAAGGAGGCCAGTGAAGTGAAGAAAGAAACAGTCAAAACC- 2621
QY 2523 ATCAAAATATATTTGTCTGAGGCAAGCCCACTTTGTCATATCTGATCAAAAGTTCAAGC 2582
DB 2622 --ACACATTTGGGGTGAATGAGCGCTGTGTCTATATCCCTTATGATGTCAAGGTCCAAGC 2679
QY 2583 CTTGATGATCATGAGGTTTGGCCCGAGCCAGCTGTAGTATGAGCAATTTCTGAGAAAG 2642
DB 2680 TATCATATCAATGAGATCTGGGCTGAGCCCTGATCAATGATCTCTAATTTCTGAGAAAG 2739
QY 2643 CTTCCCAATGTGTCTCTGAGGAAAGTGTGTGATGTGTGAAACAGTACTTGAAGCCGA 2702
DB 2740 CTATCTTAATCAAGCTCAAGTATCATGTGGGTGACCTTTAAACAGTATCAATTTAGTTAA 2799
QY 2703 GGTGACCTGGAGCCAGTACCTGTGAAGAAAGATCCGAAGAACCTTAAGAGGTATCGAT 2762
DB 2800 AGTTACTGTGTCAAGATTTCCAAAGACAGAGTACATGAGCTTGAAGAGGCTTATCAAGT 2859
QY 2763 TTAATTAATGAAGACCAAGATTTCACTTAAAGAAACAGAGTCACTATGAAGAAAGAT 2822
DB 2860 AAATTTGTGAGAAACAAAGATCTGTGTGAGAGAAACATCTCCAAAGAGTGAACAT 2919
QY 2823 CTTACCTTCCAGAGCAAGATCATGAGATGTGCTGGGCTGAGAGCCCTTTAGGCA 2882
DB 2920 TCTAAGATTTTCAAGAACAAAGAACTGTGAATGTCTTCTTGAATGTCTTTTATGGA 2979
QY 2883 CTACACACTGAATGTCCAGTGTGATGAATGGAAGAGGAGGCCAGCCAGCTGACAG 2942

DB 2980 ATTTCATTAAAGCTCTTAGACCTATATCTTAAAGAGCTGCTCGAAGATGAGCCTTA 3039
QY 2943 AGCTTTAATATCTCCGAAGAGAGTCCCCAGTGTCTCCCTGCTTTGAAGATTTGTGATCC 3002
DB 3040 TATATTTCACCAACGAGAGAGTACCTGAACCAACTTTTCTAAGGTATCAAAAGT 3099
QY 3003 AACACTGAGCTCTCTCACTTTGGATGGATCCAGGAGCAACCCGAATGGCATTTTGGAC 3062
DB 3100 TGTATTAAGACACCTGCACTTTATCTTGGGACCTAAGAAATTAATGGAAACTTAAC 3159
QY 3063 AGAGTACACCTTAAAGTATCAGCAATTAACAGACACATGAATTAAGCCCTCTGTGTA 3122
DB 3160 TGGCTATCTTTTCAATATCAGATTAATTAATGACACCTAGAGATTGAGAAATTAATGA 3219
QY 3123 TTTGAAATTT---CTGCCAAGACAGAGTGGTGGACTTTAAATTAATTTGAGAC 3179
DB 3220 TATTTACATTACCACTCCATCAAGCCAGCTGGCACTCTCAAACTGAAATGCAACTAC 3279
QY 3180 TCGATTAAGTTTATTTCTATGCAAAACATCAGAGATCAGAAATCAATTTACAGA 3239
DB 3280 CAAGTACAAATTTCTACTTGAAGGCTTGCACTTACAGGGCTGTGAAAAACCATCAAG 3339
QY 3240 GGAA 3243
DB 3340 GGAA 3343

RESULT 14

US-10-435-751-176
; Sequence 176, Application US/10435751
; Publication No. US2004005348A1
GENERAL INFORMATION:
; APPLICANT: Agensys, Inc.
; APPLICANT: Paris, Mary
; APPLICANT: Chailita-Bid, Pia M.
; APPLICANT: Jakobovits, Aya
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Ge, Wangmao
; TITLE OF INVENTION: Nucleic Acids and Corresponding Proteins
; TITLE OF INVENTION: Entitled 282P13 Useful in Treatment and Detection of Cancer
; FILE REFERENCE: 51158-20084.00
; CURRENT APPLICATION NUMBER: US/10/435,751
; PRIOR FILING DATE: 2003-05-09
; PRIOR APPLICATION NUMBER: 60/404,306
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: 60/423,290
; NUMBER OF SEQ ID NOS: 208
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 176
; LENGTH: 7650
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-435-751-176

Query Match 11.4%; Score 469.6; DB 13; Length 7650;
Best Local Similarity 48.8%; Pred. No. 1,1e-127;
Matches 1465; Conservative 0; Mismatches 1509; Indels 30; Gaps 6;
QY 243 ACAGCTCCAAACATCAACCAACAGTCTCCAAAGATTACATATTATGACCTCGGAGAA 302
DB 367 ACAGGTTCCAAACATCAATAAACAGTCAAAAGTCCAAAGTTCCTTCCCTTGATAGTA 426
QY 303 TATTTATATCCAGTGTGAAGCCAAAGGAAACGCCCCAAGCTTTTCTGACCCGTAA 362
DB 427 TTTTCAATGATGATGAGCTAAAGGAATCCAGAACCAATTTTCGGGACTAAGGA 486
QY 363 TGGAGCTCATTTGGACATGATAAAGACCTCTGTGTCACCATGAAGCTGGCAGAGAAAC 422
DB 487 TGGCAACCCCTTTTATTTCACTGACCATCGATTAATTTCCATCGAACATTTCAAGA----- 541
QY 423 GCTCATTAATTAACATATATGAGGAAGGAAGCTGAAGCTATGAAGAGTATCAAGTG 482

DB 542 ----ACATTACAGATCCCAACGAGGGGACATATCTCACTTCAAGGAAATACCGCTG 597
QY 483 TACAGCAAGAGACGAGCGGAGCTGCAGTTTCTAATAACATGTTGTCGCCCATTCAG 542
DB 598 CTTTCTTCAATTAATACCTGGGAATGCTATGTGACAGAGAAATAGATTTATATGTTCCAG 657
QY 543 ATCAACATTTGTGACCAAGAAAGAACTTGAACCAATCAACATTCAGAGTGTGAGCTTTT 602
DB 658 TGTTCGAAACCTCCAAAGAAAGAAATTTGACCTCTTGAAGTGAAGGAGATCCAAAT 717
QY 603 AGTACTTCCCTGACAGACCCCAATTGATTAACACCACTATATATTTTGGATGATTA 662
DB 718 TGTCTCCCATGCAATCTCCCAAGGCTCCCACTTTTACACATTTATGATTAATAT 777
QY 663 TTTCTTTCAAGACTTCCAAAGAGAGAGTTCGAAGTTTGAATGGGGACCTTTA 722
DB 778 TGAATTTGAACATATGAAAGATGAAGATATATATGAGCCAAAGGAGATCTATA 837
QY 723 TTTTTCATATGCTCTCCAGAGACACCCGGAAGACTATATCTGTTATGCTAGATTAA 782
DB 838 CTTGCAAAACGTGAGAAAGAAAGAGACATGCAATGACTATGCTTTGCTGCACTTCC 897
QY 783 TCATACCTAAACCATACAGAGAGCAACTATTTTCTGTGAAGTATTCAGTGAATGA 842
DB 898 AAGATTAAGACTATTTGTACAGAAATATGCAATGAATCAACAGTTTAACAGTTAAAGCA 957
QY 843 ATTGAATGACATATATGCTGCTAATTTGATGACACTGATGTTTATGATGCTAATTCAG 902
DB 958 TGTCTATGACTCAGATTCATCCAGAAATGTTTCAAGGCAATTCATACAGCAAA 1017
QY 903 TAGAGAGAGGCGACCAACATTTTAACTCCAGAGCAATGCAATGAACAAAGAGAAAT 962
DB 1018 AAAACCCAAACGTGCTGTTGCTCCCACTGAGAGTGGAGTGTTCATATACATCT 1077
QY 963 AAGAGAAATGTGCTTTCACTGAGTGTGATGAGAGAGTGTGCTTACCCCAATTTATTA 1022
DB 1078 CAAGGGGAAATCTTGCTGCTGAGTGTGTTGCTGAAGGCTTGCCAACTCCACAGGTGA 1137
QY 1023 CTGGCAAGAGAAATGGAATGCTTACCAAAACAGACATTTAATGAATTTAGAA 1082
DB 1138 TTGGAACAAATTTGTGTGACTTACAAAGGGGAGAAACAAAGAAATTTATGAGCA 1197
QY 1083 AACCTTGACATCATTTATGTTTCAAGAGCACTGTGAAATTTCAATGATATAGCAAA 1142
DB 1198 GACTTTGAAGATAGAAATGTCTCTTACAGAGCAAAAGAAATTTATGCTGACAGCCAG 1257
QY 1143 AAATGATTAAGAGCATTCACCATTAATTTCTGTGAAGTTAAAGCGCTCCATCTG 1202
DB 1258 CAATTTCTTGGAAACAGCACACTACGATTTTACGTTATAGTAAGAGACCTCTCGCTG 1317
QY 1203 GATCAGAGCCCTCAAAATCTTGTGCTGTCCCAAGAGAGATGGGACCTTGATGAG 1262
DB 1318 GACAAAGAGCTCTAGAGTGTGTATAGACACCGGAACATGTGCATTTGTATATGGA 1377
QY 1263 AGCTATGGCAACCCCAACCCAGATTAAGTGTGTTAACTAATGAGTCCCAATGAAAT 1322
DB 1378 GGTGTAAGAGAACTTCAACCAATCAATGAGTGAAGTCAATGCTCCCAAGTTGACAA 1437
QY 1438 TCAATCAATTTG---CTGTGATGTTGCTTCCCAAGGAAATCAATTTTACCACTTCA 1494
DB 1383 AGAAAGATCAAGTCAATATATCAATGATGATGCTTATGATATGATATTTATCTGGC 1442
QY 1495 ACCAAATATATCTGCTGTGTACAGTGTGAAGCTCAATGTCCATGTGAATCTTCTGC 1554
DB 1443 AAAGCATTTGTAATGCTGTGAGAGCAACAGAAATCTCAACCTGCAACACACT 1502
QY 1555 CAATGCAATATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1614
DB 1503 CTACAGGCTATTTGCAACAGGCTGCTTTAAGTATGATGATGATGATGATGATGATGAT 1562

Db 1615 TTACGCTACAGTGGTGGGTACAGTCTTTCTTACATTTGGAGTTCTTTGCTTACCTGA 1674
 Qy 1563 CCCAACCATGAGTGGTTTAAAGAGTAAAGAGTGGCTTTCATGAGATATTATTATG 1622
 Db 1675 GGGAGTGTGTCTCTGGCAGAGGTGAGAGTGAACCTCTGGAGGCGGCGTATCA 1734
 Qy 1623 TTACATGAAATGAACTTTGGAAATCAAAAGATGTACATGATGTTAAAGAAATTC 1682
 Db 1735 TATCTATGAAATGGCAGATTTGAGATCAACAGACCGAGAAAGATGTGGCTTA 1794
 Qy 1683 TGTGGCCCAAGAGCAGTACAGAACTTATAGTGTGGTGGCAGAGATTAATTAAGGAT 1742
 Db 1795 CTCATGTTGGTGAATGCTATAGGAAATCTGACATGACCGCAATTTGGATATTG 1854
 Qy 1743 GGCAGAAATGAGTTCACTTACAGCCCGAATATGAGTGTGGCAAGAGGAGCATGGT 1802
 Db 1855 AATGCTACAAATCTTAAAGTTCTCTTAAGAAATCTCGTATCCCAATTTGATATGCT 1914
 Qy 1803 GTTCCTTGAATGCAAGTGAATGAAATGATCAACCTTATCCCTCACTGTCTGTGGCTGA 1862
 Db 1915 TGAATTTACATTTGAAAGAAATGTGACATTTGAACAAGTTGAAGTTGCTG 1974
 Qy 1863 GGAACAAGAGAACTGCCAGTATGAAGTTCACTGTGACAGATCATTAAGTGT 1922
 Db 1975 GAGTAAAGATGGAAAGCTTTGA-----AATTAATGGCAGAAAGATGGCAGAT 2025
 Qy 1923 AGCTGATGTACAGTACAGTACAGCGGAGCTTACAGTGTGTGGCAACCACTGTGGA 1982
 Db 2026 AATTTATTTGAGTGAATTTGACATTTTACATTTAATTTAATTTAAGAGACCAAGTATTTA 2085
 Qy 1983 CAGCGTCTCGCAGCGGCTGTGTAGCGTTGTGTCTTCTACTCAATCTCAGCTCCGT 2042
 Db 2086 CTGCTTTCAAGTCAATAGTCTCTAGACAGTGTGCGAAT---TAACTCAAGTAACTGT 2142
 Qy 2043 TTACGATGTCCCAATCTCTCTTTGACTTAAGTACAGATCAACTTGAAGAAAGT 2102
 Db 2143 TCTTGTATGTTCCGAGTCCACAGAAACCTTCACTTGTGAAAGCAGAAAGAGTGT 2202
 Qy 2103 TCAGCTGATGGAACCCAGGCGATGACAAATATCCCATTTACAAATTTCTATCTGA 2162
 Db 2203 TCGGCTGACCTGGAGAGTGGAGCTGACCAACACAAATTTAGGAGATTAATTTGA 2262
 Qy 2163 ATATGAAGATGCAATGCAAGCCAGGCTGTGGCACAACCAATGAAATTTTGAAC 2222
 Db 2263 ATTTGAAGAGAAACAAAGAGAGCTTGAAGTGGAGAGATGACAGAGTCCAGAGAA 2322
 Qy 2223 AAGAGCCAGAGCCAGCTGAAGCTGTCTCTTACGTGAATCTACTCTTCCGCTGATGGC 2282
 Db 2323 GAAACACAGATATCTTACCTTTGGCTCATTTTGAAGATACAGTTCAAGGCTCATAGC 2382
 Qy 2283 AGTGAACAGATTTGGAGAGAGCTTGGCCAGCGGCTGTGAGCAATTTTGAAGAAC 2342
 Db 2383 CCGTGAACGAGTGAAGAGTCAAGCTTACGCGCTGACAGACATCATGAAACACACCC 2442
 Qy 2343 CTCAGAACAGATTAATAACCCCAAGCTGTGGAAGATCGGATCGAGCTGATTAATTT 2402
 Db 2443 AGAGCTCCAGATGAGATTCACAAATTAAGGCTTCAAGCTTCAACCCAGAGAAAT 2502
 Qy 2403 GAGATTTACGTGAGAGCTTGAATGTTTGAATTAATTTGAGCGCCCTTCACTGA 2462
 Db 2503 GATTAATAAGTGGAGCTTTGAAATTCATGAGCAGAAATGACAGGCTTGAAGTACAG 2562
 Qy 2463 AGTGAAGTGGCGCAGAAAGATGATGATGAATGAGATCTGTGTGTGGCAATGT 2522
 Db 2563 AGTGAAGTGGAGCCAGAGAGCCCGAGTGGTGGAGAAAGAAACAGTCAACCAAC- 2621
 Qy 2523 ATCAATATATTTGTCTCAGGACGCAACCTTTGTTCAATCTGATCAAAAGTTCAGGC 2582
 Db 2622 --ACATATTCGGGTATGACGCTGTGTATGCTTATGCTTATGATGTCAAGTCCAGGC 2679
 Qy 2583 CCGTAATGACATGGGTTGGCCCGCAGCGAGCTGATGATGAGCAATTTGGAGAGA 2642
 Db 2680 TATCATCAATGAGATCTGGGCTGACCTCAGTCAAGTCACTCTATTTCTGAGAGAA 2739

Qy 2643 CCTCCCAATGATGGTCTCGGAGACGTGCTGTGAATGTGTGAACAGTACCTTGAACCGA 2702
 Db 2740 CTATCTCTGATACAGCTCCAGATGATCATGGGGTGAACGTTTAAACAGTACATTGTTAA 2799
 Qy 2703 GGTGACCTGGAGCCAGTACCTTGAAGAACATCCGAGACACTTCAAGAGCTTATCGAT 2762
 Db 2800 AGTTACTGTGTCAACAGTTCCAAAGACAGAGTATCATGACGTCTGAAAGGCTTACAGAT 2859
 Qy 2763 TTACTATTGGAAGACCCAGATTTCTTAAAGAAACAGAGCTCATTTGAGAAAGAT 2822
 Db 2860 AATTTGTGGAAGCAAAAGTCTGTGTGATGGAAGAACACATCCCAAGAGTGAACAT 2919
 Qy 2823 CCTCACTTCCAGGACAGCAAGTCAATGAGCATTTGGCCGGGGCTAGAGCCCTTGAACCA 2882
 Db 2920 TCTAAGATTTTACAGCAAAAGAACTGTGAATGTGTTCTTCTTATGATGCTTATAGTGA 2979
 Qy 2883 CTACACACTGAATGTCCAGTGTGATGGAATGGAAGAGGAGGCGCAGCCAGCTGACAG 2942
 Db 2980 ATTTCAATTTAAGCTTATGAGCTTATTAATCTTAAAGAGCTGTGCTGAAAGTGAACCTTA 3039
 Qy 2943 AGCTTTTAACTCTCAGAAAGAGTCCAGAGTCTCCCTGCTTGTGAAGATTTGAATTC 3002
 Db 3040 TATATTTCAACACAGAGAGAGTACCTGAACAGCACTTTTTPAAGGTATCAAAAGT 3099
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 Db 3340 GGAA 3343

RESULT 15
 US-10-435-751-182
 ; Sequence 182, Application US/10435751
 ; Publication No. US20040053348A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Agensys, Inc.
 ; APPLICANT: Faris, Mary
 ; APPLICANT: Chailita-Bid, Pia M.
 ; APPLICANT: Jakobovits, Aya
 ; APPLICANT: Raitano, Arthur B.
 ; APPLICANT: Ge, Wangmao
 ; TITLE OF INVENTION: Nucleic Acids and Corresponding Proteins
 ; TITLE OF INVENTION: Entitled 282P103 Useful in Treatment and Detection of Cancer
 ; FILE REFERENCE: 51158-20084.00
 ; CURRENT APPLICATION NUMBER: US/10/435,751
 ; PRIORITY FILING DATE: 2003-05-09
 ; PRIOR APPLICATION NUMBER: 60/404,306
 ; PRIOR FILING DATE: 2002-08-16
 ; PRIOR APPLICATION NUMBER: 60/423,290
 ; NUMBER OF SEQ ID NOS: 208
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 182
 ; LENGTH: 7650
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-10-435-751-182

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 22, 2004, 21:48:06 ; Search time 9787 Seconds
(without alignments)
12613.697 Million cell updates/sec

Title: US-09-301-380-1
Perfect score: 4134
Sequence: 1 cttcaagttcccgcatga.....tggtagagagatatttc 4134

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues
Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estcov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estcom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
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25: em_gss_rtd:*
26: em_gss_phg:*
27: em_gss_vrt1:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2265.4	54.8	4178	11	AK087693 Mus muscu
2	647.8	15.7	2394	11	AK045259 Mus muscu
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4	631.8	15.3	639	9	AL134791 DKFp547K

5	628.8	15.2	3166	11	AK048567 Mus muscu
6	625.6	15.1	639	14	CB294617
7	615.4	14.9	806	13	BU615094
8	603.6	14.6	794	14	CF533313
9	602.4	14.6	757	13	BU612550
10	601.4	14.5	824	14	CA327466
11	598.8	14.5	752	14	CF741342
12	598.8	14.5	3037	11	AK052440
13	580.4	14.0	753	14	CA316157
14	553	13.4	594	13	BX505499
15	551.8	13.3	775	14	CD804797
16	549.6	13.3	800	9	AU130055
17	548	13.3	998	13	BQ715777
18	545.4	13.2	943	13	BU505113
19	544.4	13.2	726	14	CF737303
20	536.6	13.0	962	13	BU504945
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22	531	12.8	826	13	BU604950
23	528.2	12.8	670	14	CF173249
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25	519.2	12.6	733	12	BI739003
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29	502.2	12.1	732	14	CB249525
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31	492.8	11.9	688	12	BM963623
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35	465.8	11.3	693	13	BQ308392
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43	450.4	10.9	751	14	CB452222
44	448.2	10.8	725	13	BU350956
45	439	10.6	4919	11	BC040674

ALIGNMENTS

RESULT 1
AK087693
LOCUS
DEFINITION Mus musculus 2 days pregnant adult female ovary cDNA, RIKEN
full-length enriched library, clone:R330007H08 product:NRCA
PROTEIN homolog (Homo sapiens), full insert sequence.
ACCESSION AK087693
VERSION AK087693.1 GI:26104446
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE
1 Carninci, P. and Hayashizaki, Y.
High-efficiency, full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
MEDLINE 99279253
PUBMED 10349636
TITLES
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
JOURNAL MEDLINE 20499374
PUBMED 11042159

REFERENCE	3	Shibata, K., Itoh, M., Aizawa, K., Nagoaka, S., Sasaki, N., Carninci, P., Komio, H., Akiyama, U., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Suni, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kaishiwagi, K., Fujiwaka, S., Inoue, K., Togawa, K., Izawa, M., Ohara, E., Watabiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsunura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kiru, A. and Hayashizaki, Y.
JOURNAL		RIKEN Integrated Sequence analysis (RISA) system-384-format
MEDLINE		Genome Res. 10 (11), 1757-1771 (2000)
PUBMED		20530913
REFERENCE	11076861	
AUTHORS	4	The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
TITLE		Functional annotation of a full-length mouse cDNA collection
JOURNAL		Nature 409, 685-690 (2001)
REFERENCE	5	
AUTHORS		The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
TITLE		Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL		Nature 420, 563-573 (2002)
REFERENCE	6 (bases 1 to 4178)	
AUTHORS		Adachi, J., Aizawa, K., Akimura, T., Arai, A., Hoshizume, W., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hayashida, K., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Horii, F., Imocani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Komori, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Ohno, M., Ohseto, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.
TITLE		Direct Submission
JOURNAL		Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gs.riken.go.jp, URL: http://genome.gsc.riken.go.jp, Tel: 81-45-503-9222, Fax: 81-45-503-9216)
COMMENT		cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
		Please visit our web site for further details.
		URL: http://genome.gsc.riken.go.jp/
		URL: http://fantom.gsc.riken.go.jp/
FEATURES		Location/Qualifiers
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		/db_xref="MGI:24263104"
		/db_xref="taxon:10090"
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		/clone_lib="RIKEN full-length enriched mouse cDNA library"
		/dev_stage="2 days pregnant adult"
		1..4178
		/note="NR CAM PROTEIN homolog [homo sapiens] (SPTP 015179, evidence: FASSTY, 95.3%ID, 18%length, match=705)"
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Query Match	54.8%	Score 2265.4; DB 11; Length 4178;
Best Local Similarity	83.1%	Pred.No. 0;

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QY	60	TTTGTGAAAGAAAGAAAGAAATTCACGTGTGTGAGTCTCAGCAGAGTTAAAGTAATGCA	119							
Db	440	TCCTGAGAGAGAGAAAGAAATTCCTGTGTGTGTCTCAGCAGAGTGTGACGTGATGCA	499							
QY	120	GCTTAAATATATGCGGAAAAAGAGCGCTTATCTGCGGAGAGTGTGCTGATTTCTT	179							
Db	500	GCTTAAATATATGCGGAAAGAAAGCACTTATCTGACGAGCGAGTGTGCTGATTTCTT	559							
QY	180	CCCTGTGCAGATGATTTAGTGTGACCTGGAAGTAACTCTTGATCCAAAATCTTGAAAGCTT	239							
Db	560	CCCTGTGCAGATGATGACGCGGTGATGTTCTCTTGATC-----T	601							
QY	240	GGTACAGCTTCAACCATCAACCCCAACAGTCTCCAAAGATTAATTAACCTCGCGGA	299							
Db	602	GGTACACCTTCAACCATCACTCACTCAACAGTCAACCAAGATTAATTAACCTCGCGGA	661							
QY	300	GAATATTGTATCCAGTGTGAAAGCCAAAGGAGAAACGCGCCCAAGCTTTTCTGTGACCG	359							
Db	662	GAATATTGTATCCAGTGTGAGGCAAAAGGAGAACTCCCAAGCTTTTCTGTGACTCG	721							
QY	360	TAAATGGAGCTCATTTTGAATCCATTAAGAACCTCTGTGTCAACCATGAAGCTTGCACAG	419							
Db	722	TAAATGGAGCTCATCTTTGACATTAAGAACCCCTGTGTCAACCATGAAGCTTGCACAG	781							
QY	420	AAGGCTCATATTAACCATCATGAGCGAAGGAGAAAGTGAAGCCATATAGAGAGCTATCA	479							
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Db	842	GTTGACAGCAAGAGAGCGGAGGTGAGCTGCGGTCTCAATTAACGTTGTGTGCGCCATC	901							
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| | | | |
QY 3209 CATGACAGATCAAGAGTCAAAATTTACAGAGAGAGAGATTAACAACTGTGATGAGT 3267
| | | | |

Qy	475	TATCAGTGAACGCAAGGACGAAGCGGAGCTGCAGTTCTTAATPAACAATTGTGTCCG	534
Db	586	TACCACTGCACTGCAGAGACGAGCGTGAAGCTGCCCTCTCCAAATPACATTGTGTCCG	645
Qy	535	CCATCCAGATCACCAATTGTGAGCCAAAGAAAACTTGAACCAATCACACTTCCAAAGTGT	594
Db	646	CCATCTAGGTCACTCTGTGGACCAAGGAAAACTTGAACCAATCTATGTACTCCAGAAATGG	705
Qy	595	CAGCTTTAGTACTCCCTGCAGACCCCAATTGGAATTAACCAACCCTATATATTTGG	654
Db	706	CAGTATTAGTACTTCCATGTAAGCCTCCGATTGATTAACCTCCGGCCATATATTTGG	765
Qy	655	ATGATTAATTCCTTTCAAAAGACTTCCACAAAGTGAAGAGTTTCTCAAGTTTGAATGG	714
Db	766	ATGATTAATTCCTTTCAAGACTTCCACAAAGTGAAGCGGTTTCCCAAGGCTTAATGGA	825
Qy	715	GACCTTTATTTTCCAAATGTCTCTCCCAAGGACACCCCGGAAGACTATATCTGTATGCT	774
Db	826	GACCTTTACTCTCCAAATGTCTCTCCCAAGGACACCCCGGAAGACTATATCTGTATGCT	885
Qy	775	AGATTATATCACTCAAAACCATACAGCAGAGAACCAACTTCTGTGAAGGTGAATTTCA	834
Db	886	AGATTATATCACTCAAAACCATACAGCAGAGAACCAACTTCTGTGAAGGTGAATTTCA	945
Qy	835	GTGATGAATGAATGACACTTAATGCTGTAAATTTGAGTGACACTGAGTTTATGTGCT	894
Db	946	GTGATGAATGAATGACACTTAATGCTGTAAATTTGAGTGACACTGAGTTTATGTGCT	1005
Qy	895	AAATCA 900	
Db	1006	GAGTTA 1011	

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FEATURES
SOURCE

RESULT 3
CF737289
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

CF737289 788 bp mRNA linear EST 10-OCT-2003
UT-M-HD0-ckr-1-15-0-UT.r1 NIH_BMAP_HD0 Mus musculus cDNA clone
IMAGE:30610358 5', mRNA sequence.
CF737289
CF737289.1 GI:37633625
EST.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 788)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. James Lin University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/mouseefl.html
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)
Seq primer: PYX-5.
Location/Qualifiers
1..788

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location/Qualifiers
1..788
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:30610358"
/tissue_type="whole eye"
/dev_stage="embryo_12.5,13.5,14.5 dpc"
/lab_host="DH10B (T1 phage resistant)"
/clone_1b="NH_BMAL_H00"
note="Organ: Eye; Vector: pYX_Asc; Site_1: EcoR I"

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Site 2: Not I. The library was constructed according to Bonafide, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with NotI and then cloned directionally into pX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is TTATTGAGGT. This library was created for the University Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH)."

Query Match	15.34;	Score 632.2;	DB 14;	Length 788;
Best Local Similarity	88.23;	Pos. No. 1.9e-164;		
Matches 696;	Conservative 92;	Mismatches 94;	Indels 1;	Gaps 14;
QY 833	CAGNGGATGGAATTGAATGACCTPAGTGTGTAATTTAGAGACACTGAGTTTATGSGT			892
Db 1	CAGTGGATGGAATTAATGACCTATAGTGTCTAATTTAGAGACACTGAGTTTATGSGT			60
QY 893	CTAATATCAAGTAGAGAGAGGCCCAACCATTTTAACTCCGAAGAGCAATCAAGTAACA			952
Db 61	CTAATATCAAGTAAGAGAGAGGCCCAACCATTTTAACTCCGAAGAGCAATCAAGTAACA			120
QY 953	AAGAGGAATTAAGAGGAATGTGCTTTCACTGAGTGCATTTGCAAGAGACTGCTTACC			1012
Db 121	AAGAGGAATTAAGAGGAATGTGCTTTCACTGAGTGCATTTGCAAGAGACTGCTTACC			180
QY 1013	CAATTAATTTACTGGGCAAAAGGAATGGAATGCTAACCCAAAACAGGACATTTATAGA			1072
Db 181	CAATTAATTTACTGGATCAAAAGGAATGGAATGCTAACCCAAAACAGGACATTTATAGA			240
QY 1073	ACTTTGAGAAAACCTTGACGATCAATTCATGTTTACAGAAAGACACTGGAATTAACAAT			1132
Db 241	ACTTTGAGAAAACCTTGACGATCAATTCATGTTTACAGAAAGACACTGGAATTTATCAAT			300
QY 1133	GTATAGCAAAAATATGATTTAGAGACCAATCCACATACCATTTCTGTTAAGCTTAAAGCG			1192
Db 301	GCATAGCAAAAATATGATTTAGAGACCAATCCACATACCATTTCTGTTAAGCTTAAAGCG			360
QY 1193	CTCCATATCTGGATTAACAGCCCTCAATAATCTTGTGCTGTCCCAAGAGAGATGGAGCT			1252
Db 361	CTCCATATCTGGATTTGTGGCACTTCAATAATCTTGTGCTTCCCAAGAGAGATGGAGCT			420
QY 1253	TGATCTCAGAGCTAATATGGCAACCCCAACCCCAATTTAGTGTGTTAACAATGGAGTCC			1312
Db 421	TGATCTCAGAGCTAATATGGCAACCCCAACCCCAATTTAGTGTGTTAACAATGGAGTCC			480
QY 1313	CAATAGAAATTTGCCCTCGATGACCCCGACAGAAAATATGATGGGATACCATTAATTTT			1372
Db 481	CAATAGAAATTTGCTCTCGATGACCCCGACAGAAAATATGATGGGATACCATTAATTTT			540
QY 1373	CAAAATGTTCAAGAAAGATCAAGTCAAGTATATCAATGCAATGCTCTTAATGAATATGAT			1432
Db 541	CAAAATGTTCAAGAAAGATCAAGTCAAGTATATCAATGCAATGCTCTTAATGAATATGAT			600
QY 1433	ATTATATCGGCAAAAGCATTTGTAAATGTGTGTGCTGAGCCACACAGAAATCTTCAACCTG			1492
Db 601	ATTATATCGGCAAAAGCATTTGTAAATGTGTGTGCTGAGCCACACAGAAATCTTCAACCTG			659
QY 1493	CAAAACACACTTACAGAGTCAATGCAAAAGAGGCTGCTTTACTAGACTGTGCTTCTTGT			1552
Db 660	CAAAACACACTTACAGAGTCAATGCAAAAGAGGCTGCTTTACTAGACTGTGCTTCTTGT			719
QY 1553	GGTCTCTCTCCCAACCATCGAGTGTTTAAAGAGCTAAAGGAAGTCTTTCATGAAG			1612
Db 720	GATCTCTCTCAAGCATTTGAGTGTAAAGGCACTAAAGGAAGGCTTTCATGAAG			779
QY 1613	ATATTTATG 1621			

Db 780 ACATTATG 788

RESULT 4
AL134791 639 bp mRNA linear EST 04-SEP-2003
LOCUS DKFZP547K0690.1 547 (synonym: hfbp1) Homo sapiens cDNA clone
DEFINITION DKFZP547K0690.5, mRNA sequence.
AL134791
ACCESSION AL134791.1 GI:6602978
VERSION EST.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 639)
Poultka,A., Wellenreuther,R., Mewes,H.W., Weil,B. and Wiemann,S.).
EST (Poultka,A., Wellenreuther,R., Mewes,H.W., Weil,B. and
Wiemann,S.)
JOURNAL Unpublished (1999)
COMMENT
MIPS
Ingolstaedter Landstr.1, D-85764 Neuberberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email: s.wiemann@kfz-heidelberg.de;
sequenced by DKFZ (German Cancer Research Center,
Heidelberg/Germany) within the cDNA sequencing consortium of the
German Genome Project.
No 31 sequence available.
This clone (DKFZP547K0690) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
Location/Qualifiers
1. 639
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZP547K0690"
/issue_type="brain"
/dev_stage="fetal"
/lab_host="X1-2blue"
/clone_1ib="547 (synonym: hfbp1)"
/note="Vector: pAMP1, Site_1: NotI; Site_2: SalI"

ORIGIN

Query Match 15.3%; Score 631.8; DB 9; Length 639;
Best Local Similarity 99.5%; Pred. No. 2.2e-164;
Matches 633; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

1013 CAATTATTACCTGGGGAAGGAAGATGCTACCCAAAACAGAGACGTTTATTAAGA 1072
|||||
1 CAATTATTACTGGGCAAGGAAGATGCTACCCAAAACAGAGACGTTTATTAAGA 60
|||||
1073 ACTTTGAGAAAACCTTGAGATCATGTTTCAGAGAGAGACTGTGAAATTACCAAT 1132
|||||
61 ACTTTGAGAAAACCTTGAGATCATGTTTCAGAGAGAGACTGTGAAATTACCAAT 120
|||||
1133 GTATAGCAAAAAATGCAATTGAGAGCAATCCATTCATTTGTTAAGATTAAAGCG 1192
|||||
121 GTATAGCAAAAAATGCAATTGAGAGCAATCCATTCATTTGTTAAGATTAAAGCG 180
|||||
1193 CTCCTACATGAGATCAGAGCCCTCAAAATCTGTGTCGCCAGAGAGAGATGGAGCT 1252
|||||
181 CTCCTACATGAGATCAGAGCCCTCAAAATCTGTGTCGCCAGAGAGAGATGGAGCT 240
|||||
1253 TGATCTGACAGAGCTAATGGAACCCCAAAACCAAGATTAGCTGTGAAGATGAGCTC 1312
|||||
241 TGATCTGACAGAGCTAATGGAACCCCAAAACCAAGATTAGCTGTGAAGATGAGCTC 300
|||||
1313 CAATAGAAATTGCTGATGATGACCCAGCAGAAAAATAGATGGCATACATTATTTT 1372
|||||
301 CAATAGAAATTGCTGATGATGACCCAGCAGAAAAATAGATGGCATACATTATTTT 360
|||||

Qy 1373 CAATGTTCAAGAAAGATCAAGTGCATATATCATGTCGAATGCTCTAATGAAATGAGT 1432
|||||
Db 361 CAATGTTCAAGAAAGATCAAGTGCATATATCATGTCGAATGCTCTAATGAAATGAGT 420
|||||
Qy 1433 ATTTACTGGCAAAAGCATTTTGAATATGTCGCTGAGACCCACAGCAATTCCTACACCTG 1492
|||||
Db 421 ATTTACTGGCAAAAGCATTTTGAATATGTCGCTGAGACCCACAGCAATTCCTACACCTG 480
|||||
Qy 1493 CAACACACTTACACAGGTCATGCAACAGGCTGCTTTACTAGACTGTGCTCTCTTG 1552
|||||
Db 481 CAACACACTTACACAGGTCATGCAACAGGCTGCTTTACTAGACTGTGCTCTCTTG 540
|||||
Qy 1553 GGTCTCTCTCCCAACATGAGTGTGTTAAAGAGCTAAAGAAAGTCTTCAATGAAG 1612
|||||
Db 541 GGTCTCTCTCCCAACATGAGTGTGTTAAAGAGCTAAAGAAAGTCTTCAATGAAG 600
|||||
Qy 1613 ATATTATGTTTATCATGAAATGGAACCTTGGAAA 1648
|||||
Db 601 ATATTATGTTTATCATGAAATGGAACCTTGGAAA 636
|||||

RESULT 5
AK048567 3166 bp mRNA linear HTC 20-SEP-2003
LOCUS AK048567
DEFINITION Mus musculus 16 days embryo head cDNA, RIKEN full-length enriched
library, clone:G130076007 product:NRCAM PROTEIN homolog [Homo
sapiens], full insert sequence.
AK048567.1 GI:26339411
VERSION AK048567.1
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
1
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
MEDLINE 99279253
PUBMED 10349636
REFERENCE
AUTHORS
TITLE
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
JOURNAL 2049374
MEDLINE 11042159
PUBMED 11042159
REFERENCE
AUTHORS
TITLE
Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
Konno,H., Akiyama,J., Nishi,K., Kitasuna,T., Tashiro,H., Itoh,M.,
Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kasaiwagi,K.,
Fujiwara,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watabiki,M.,
Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsura,S., Kawai,J.,
Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
JOURNAL 20530913
MEDLINE 11076861
PUBMED 11076861
REFERENCE
AUTHORS
TITLE
The RIKEN Genome Exploration Research Group Phase II Team and the
FANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
JOURNAL 5
MEDLINE
PUBMED
REFERENCE
AUTHORS
TITLE
The FANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
JOURNAL


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/organism="Pan troglodytes"
/mol_type="mRNA"
/db_xref="taxon:9598"
/clone="12B22031_rev_1.F02_r_027.ab1"
/sex="male"
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/dev_stage="adult"
/lab_host="Epigloptarian Coli (TM) XL-10-Gold"
/clone_lib="Chimpanzee brain library Kooze"
/notes="Vector: pUC19; Site: 1: SfiI-A; Site 2: SfiI-B. The library was prepared using the SMART cDNA library construction kit (Clontech), doing only primer extension, but not PCR amplification of the cDNA. The only deviation from the published protocol was that we cloned the cDNA into a plasmid vector."

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Query Match	15.1%	Score 625.6	DB 14	Length 639
Best Local Similarity	99.1%	Pred. No. 1.2e-162		
Matches 628, Conservative	0	Mismatches 6	Indels 0	Gaps 0

OY	2142	CATTACAAATTTCAATCATCCGAATATGAGATGCAATGACAAAGCCAGGGCTGTGGACCA	2201
Db	6	CATTACAAATTTCAATCATCCGAATATGAGATGCAATGACAAAGCCAGGGCTGTGGACCA	65
OY	2202	CCAAACTGAATTTCTGGAAACACAGACCACAGCCCAAGCTGTCTCTTAAGTAA	2261
Db	66	CCAAACTGAATTTCTGGAAACACAGACCACAGCCCAAGCTGTCTCTTAAGTAA	125
OY	2262	CTACTCCTTCGCGCGATGAGCAGTGAACAGCATTTGGGAAAGCTTGGCCACGAGGCTC	2321
Db	126	CTACTCCTTCGCGCGATGAGCAGTGAACAGCATTTGGGAAAGCTTGGCCACGAGGCTC	185
OY	2332	TGAGCAGATTTTGAACGAAGCCTCAGAACCCAGATTAACCCCAAGCTGTGGAAAGACT	2391
Db	186	TGAGCAGATTTTGAACGAAGCCTCAGAACCCAGATTAACCCCAAGCTGTGGAAAGACT	245
OY	2382	GGGATCAGAGCCTGATTAATTTGGAGATTACGTGAAAGCCCTTGAATGTTTGCATCTTA	2441
Db	246	GGGATCAGAGCCTGATTAATTTGGAGATTACGTGAAAGCCCTTGAATGTTTGCATCTTA	305
OY	2442	TGGGCGAGGCGTTCACTGACAAAGTTAGGTGGGCGCAGAAAGTGGTGAATGATGAGAC	2501
Db	306	TGGGCGAGGCGTTCACTGACAAAGTTAGGTGGGCGCAGAAAGTGGTGAATGATGAGAC	365
OY	2502	ATCTGTGGTTGTGGCAAAATGATCCAAATATATTTGTCTCAGGCAAGCCAACTTGTTC	2561
Db	366	ATCTGTGGTTGTGGCAAAATGATCCAAATATATTTGTCTCAGGCAAGCCAACTTGTTC	425
OY	2562	ATACCTGATCAAAGTTCAAGGCCCTGAAATGACATGGGGTTTGGCCCCGACCACTGTAGT	2621
Db	426	ATACCTGATCAAAGTTCAAGGCCCTGAAATGACATGGGGTTTGGCCCCGACCACTGTAGT	485
OY	2622	CATGGGACATTTCTGGAGAAAGACTCCCAATGGTGGCTCTTGGGAACGTGCGTGAATGT	2681
Db	486	CATGGGACATTTCTGGAGAAAGACTCCCAATGGTGGCTCTTGGGAACGTGCGTGAATGT	545
OY	2682	GGTGAACAGTACTTACCGGAGGTCACTGGGACCCAGTACTCTGAAAAGCATCCAGG	2741
Db	546	GGTGAACAGTACTTACCGGAGGTCACTGGGACCCAGTACTCTGAAAAGCATCCAGG	605
OY	2742	ACACTTACAAAGCTATGGGATTTACTATTTGGAAG	2775
Db	606	ACACTTACAAAGCTATGGGATTTACTATTTGGAAG	639

RESULT 7	
BUG15094	
LOCUS	806 bp mRNA linear EST 20-FEB-2003
DEFINITION	UI-M-FRO-cbe-f-02-0-UI.r1 NIH_EMAP_FRO Mus musculus cDNA clone
DESCRIPTION	UI-M-FRO-Cbe-f-02-0-UI 5' NRNA sequence.
ACCESSION	BUG15094
VERSION	BUG15094.1 GI:23281321

KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
EST.	Mus musculus (house mouse)	Mus musculus	Bukayrova; Merazoa; Chordata; Craniata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus	NIH-MGC	http://mgc.nhl.nih.gov/	National Institutes of Health, Mammalian Gene Collection (MGC)	unpublished (1999)
			1 (bases 1 to 806)				Contact: Robert Strausberg, Ph.D.

This clone was contributed by the Brain Molecular Anatomy Project (BMAP).
Seq primer: pYX-5'-Gat-1-5'-G

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Location/Qualifiers
1. .806
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/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="UI-M-FR0-cbe-f-02-0-UI"
/tissue_type="whole brain"
/dev_stage="embryo 13.5,14.5,16.5,17.5dpc"
/lab_host="DH10B (T1 phage resistant)"
/clone_1ib="NIH BMAP FR0"
/note="Organ: Brain; Vector: pYX-Asc; Site:1: EcoR I;
Site:2: Not I; The library was constructed according
Bonaldi, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the poly A tail
is AGCAGACAG. This library was created for the University
Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
program coordinator."

```

Query Match	14.9%	Score 615.4	DB 13	Length 806
Best Local Similarity	85.9%	Pred. No. 9.5e-160		
Matches 693	Conservative 0	Mismatches 113	Indels 1	Gaps 1
Qy	2108	TGTCATGGACCCGAGCGATGACAAACAATAGCCCCCATTCACAAATTCATCATCGAATATG	2167	
Db	1	TGACATGATGACCCGAGGAGACGACAAACAATAGCCCCCATTCACAAATTCATCATCGATG	60	
Qy	2168	AAGATGCATGCACAGCCAGGCGCTGTGGACCCACCAACTGAAGTTTCTGGAAACACAGA	2222	
Db	61	AAGATGCATGCATGATGACAGGCGCTGTGGCCCCACAGCGCTGAAGTTTCTGGAAACACAGA	120	
Qy	2228	CCAAGGCCGAGCTGAAGCTGTCTCTTACGGAACCTACTCCCTTCGCGGTATGGACAGAGA	2287	
Db	121	CCACAGCCCAACTGAAGCTGTCTCTTATGTGAACCTACTCCCTTCGCGGTATGGACAGAGA	180	
Qy	2288	ACAGCATTTGGGAAGAGCTTGGCCCAAGCAGCGGTCTGACAGATATTTGACGAAACCTCAG	2347	
Db	181	ACAGCATTTGGGAAGATGATGCCCCGAGCAGGACATCCGAGCACTATCTTACAAAAACCCGAG	240	
Qy	2348	AACCAGATAAAACCCCAACAGCTGTGGAAAGGACTGGGATCGAGCCTTGATTAATTGGAGA	2407	
Db	241	AACCAGATCAGAAATCCCATGGCTGTGGAAAGGACTTAAGGACAGACCCGACCAACTTTGGTGA	300	
Qy	2408	TTACGTGAGACCCCTTGATAGTGTTCGCAATCTAAATGGCCACAGGCTTCAGTACAAAGTTA	246	

Db	301	TTACATGSAAGCCCTGTAATGGTTTTCAAATGGAATGGGCTCGGCTCCAGTACAAAGTGA	360
OY	2468	GCTGGCGCCAGAAAGATGGTAGATGAATGAGACATCTGTGGTGTGGCAATGATATCA	2527
Db	361	GCTGGCGCCAGAAAGATGGTAGCATGAGTGGAGCGTGTGGTGTGGCCAATGATATCA	420
OY	2528	AATATATATGTCTCAGGACGCGCAACCTTGTTCATACCTGATCAAAATTTAGGCGCTTGA	2587
Db	421	AATCATATGTCTTCGGACACCAACCTTTGTGCCATACCTATATAAAATTTAAACCTCTGA	480
OY	2588	ATGACATGGGGTTTGCCCCCGAGCCAGCTGTAGTATCATGGGACATTTCTGGAGAAAGCTCC	2647
Db	481	ATGATGTGGGTTTGTGCACCAAGACCGTAGTGCATGTGGGCAATTTCTGGAGAAAG-CTTC	539
OY	2648	CAATGTGTGCTCTCGGGAACGTGCGTGTGAATGTGTGAACAGTACCTTAGCCGAGGTGC	2707
Db	540	CAATGTGTGCTCTCGGAATATGTGGCGTCAACGTGTGTGAACAGTACCGTGGCAAGGTGC	599
OY	2708	ACTGGGACCCAGTACCTCTGAAAAGCAATCGAGACACCTTACAAAGGCTATGTGGATTACT	2767
Db	600	ACTGGGACCCAGTGTCTCTCCAAAGAGTGTCCAGAGCACTTACAAAGGCTATCGGATTACT	659
OY	2768	ATTGGAAGACCCAGAGTTCACTCTAATAAAGAAACAAGCGTCACATTTGAGAAAAAGATCTCA	2827
Db	660	ACTGGAAGACCCAGAGTCTCTCTAATAAAGAAACAAGCGGCTCACATTTGAGAAAGATCTCA	719
OY	2828	CCTTCCAAAGCAGCAAGACTCATGGCATGTTCGGGGGCTTAGAGCCCTTTAGCCACTACA	2887
Db	720	CCTTCCAGNNNCACAAAGACTCAGCGCATGTGCGCAGGGGCTCAGCCCATACAGTCACTATG	779
OY	2888	CACGTAAATGTCCGAGTGTCAATGGGA	2914
Db	780	CCCTCAACGTCCGAGTGTCAACGGGA	806

FEATURES	LOCATION	QUALIFIERS
RESULT 8		
CE533313		
DEFINITION	CE533313	794 bp mRNA linear EST 12-SEP-2003
ACCESSION	UI-M-FY0-cgt-f-05-0-UI.r1 NIH_BMAP_FY0	Mus musculus cDNA clone
VERSION	IMAGE:30363868.5,	mRNA sequence.
KEYWORDS	CE533313	
SOURCE	CE533313.1	GI:34585281
ORGANISM	EST.	
REFERENCE	Mus musculus	
AUTHORS	Mus musculus	
JOURNAL	Buxarjota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
COMMENT	Mammalia; Eutharia; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
	1 (bases 1 to 794)	
	NIH-MGC http://mgc.nci.nih.gov/ .	
	National Institutes of Health, Mammalian Gene Collection (MGC)	
	Unpublished (1999)	
	Contact: Robert Stransberg, Ph.D.	
	Email: CGAB@rs@mail.nih.gov	
	Tissue Procurement: Dr. Jim Lin, University of Iowa	
	cDNA library preparation: Dr. M. Bento Soares, University of Iowa	
	DNA Sequencing by: Dr. M. Bento Soares, University of Iowa	
	Clone Distribution: Distribution information can be found at	
	http://genome.uiowa.edu/distribution/mouse1.html	
	This clone was contributed by the Brain Molecular Anatomy Project	
	(BMAP)	
	Seq primer: PYX-5.	
	Location/Qualifiers	
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/db_xref="taxon:10090"
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/lab_host="DH10B (T1 phage resistant)"

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/clone_11b="NIH_BMAP_FY0"
 /note="Organ: Brain; Vector: pYX-Asc; Site_1: EcoR I;
 Site_2: Not I; The library was constructed according
 to Bonaïdo, Lemon and Soares, Genome Research, 6:791-806,
 1996. Denatured RNA was size fractionated on a 1% agarose
 gel. First strand cDNA synthesis was primed with oligo-dT
 primer containing a Not I site. Double strand cDNA was
 size selected according to mRNA size fraction, ligated
 with EcoR I adaptor, digested with NotI and then cloned
 directionally into pYX-Asc vector. The library tag
 sequence located between the Not I site and the polyA tail
 is AGCGAGCAGC. This library was created for the University
 of Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
 Developing Mouse Nervous System', supported by National
 Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
 program coordinator."

Query Match	Local Similarity	14.6%;	Score 603.6;	DB 14;	Length 794;
Best Local Similarity	85.5%;	Pred. 1.98-156;			
Matches	680;	Conservative	0;	Mismatches 114;	Indels 1;
Qy	838	GATGAAATTGAATGACACTATAGCTCTGCTAAATTTGAGTACACTGAGCTTTATGTGCTAA	897		
Db	1	GATGAAATTGAATGACACTATAGCTCTGCTAAATTTGAGTACACTGAGCTTTATGTGCTAA	60		
Qy	898	TCAAGTGAAGAGAGGCGCCACCAACTTTTAACTCCAGAAGGCATGCAAGTAAACAAAG	957		
Db	61	TCATGTAAGAGAGGCGCCACCAACTTTTAACTCCAGAAGGCATGCAAGTAAACAAAG	120		
Qy	958	GAATTAAGAGAAATGTGCTTTCACTGAGTGCATTGACAGAAGACTGCTTACCCCAAT	1017		
Db	121	GAATTAAGAGAAACGTGCTTTGCTGAGTGCATTGCGGAAGGCTTACCTCAAT	180		
Qy	1018	ATTTCATCGGGCAAGGAAGATGAAATCTTACCCAAAACAGACATTTATAGAATCTT	1077		
Db	181	ATTTCATCGGAATCAAGGAAGACGAATCTTCCCGCAACGGACATTTTATCGAACCTTT	240		
Qy	1078	GAGAAACCTTTCGAGATCATTCATGTTTCAAGAAACACTCTGGAATTTCAATGTATA	1137		
Db	241	AAGAAACCTTTCGAGATCATTCATGTTTCCGAAGCCACTCTGGAATTTCAATGTATA	300		
Qy	1138	GCAAAAAATGATCTTAGAGGCATTCACATACATTTCTGTAGAGTTAAAGCGCTCCA	1197		
Db	301	GCAAAAAACGATTAGAGGCATTCACATACATTTCTGTACTGTTAAAGCGGCTCC	360		
Qy	1198	TACTGATTCACAGCCCTCTCAAAATCTTGTGCTGTCCCAAGAGAGATGGACCTTGATC	1257		
Db	361	TACTGATTCGTGTGACCTCAAAACCTGCTGCTTCCCGGAGAGAAATGGGACCTTCATC	420		
Qy	1258	TGCGAGCTATATGSCAACCCCAAAACCGAATTAAGCTGTGTTAACAAATGGAGTCCCAATA	1317		
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Qy	1318	GAAATTCGCCCTGTGACCCCGACAGAGAAAATAGATGGCATAACCATTAATTTTTCAAT	1377		
Db	481	GAAATTCGTCGATGACCCCGACAGAGAAAATAGATGGCATAACCATTAATTTTTCAAT	540		
Qy	1378	GTTCAAGAAAGATCAAGTCAATATATCAATGCAATGCTCTTAATGAATATGATATTTA	1437		
Db	541	GTTCAAGAAAGATCAAGTCAATATATCAATGCAATGCTCTCTTAACANAATATGATATTTA	600		
Qy	1438	CTGGCAAAAGCATTTGTAATATGCTGGCTGAGGCCAACGAATCTTCAACACCTGCAAC	1497		
Db	601	CTAGCAATATGATTTGTAATATGCTGCTGACCACTTGGATTTCTCAATCAGCANAC	660		
Qy	1498	ACACTTACAGGATGATGCAACAGGCGTCTTTACTAGACTGTGCTTCTTTGGGTCT	1557		
Db	661	ACACTGTACAGGATGATGCAACAGGCGTCTTTGCTAGATATGTGCTTCTTTGGATCT	720		
Qy	1558	CTCTCTCCCAACCATTCAGTGTGTTAAAGAGCTTAAAGAAAGTCTCTTCAATGAAGATAT	1617		
Db	721	CTTATGCTCTT-CAATGATGTGGTTAAAGCACTAAAGAGGCTCTTCAATGAAGATATAT	779		

QY 1618 TATGTTTACATGA 1632
 DB 780 TTTGCATGATATGA 794

RESULT 9
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 DEFINITION UI-M-FRO-cdc-e-18-0-UI.r1 NIH_BMAP_FRO Mus musculus cDNA clone
 BU612550
 VERSION UI-M-FRO-cdc-e-18-0-UI 5', mRNA sequence.
 KEYWORDS BU612550.1 GI:23278765
 SOURCE EST.
 ORGANISM Mus musculus (house mouse)

REFERENCE
 AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 TITLE NIH-MGC http://img.nci.nih.gov/
 JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
 COMMENT Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgaabs-remail.nih.gov
 Tissue Procurement: Dr. Jim Lin, University of Iowa
 cDNA library preparation: Dr. M. Bento Soares, University of Iowa
 DNA library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Clone distribution information can be obtained from Dr. M. Bento Soares, bento-soares@uiowa.edu
 This clone was contributed by the Brain Molecular Anatomy Project (BMAP)

Seq primer: pyx-5.
 Location/Qualifiers
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 /mol_type="mRNA"
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 /db_xref="taxon:10090"
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 /dev_stage="embryo 13.5,14.5,16.5,17.5dp"
 /lab_host="DH10B (T1 phage resistant)"
 /clone_lib="NIH BMAP FRO"
 /note="Organ: Brain; Vector: pyx-Asc; Site 1: Bcor I; Site 2: Not I; The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction. Ligated with Bcor I adaptor, digested with NotI and then cloned directionally into pyx-Asc vector. The library tag sequence located between the Not I site and the polyA tail is AGCGAGACAG. This library was created for the University Iowa Brain Anatomy Project (BMAP). Gene Discovery in the Developing Mouse Nervous System, supported by National Institute of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."

ORIGIN
 Query Match 14.6%; Score 602.4; DB 13; Length 757;
 Best Local Similarity 87.2%; Pred. No. 3,9e-156;
 Matches 660; Conservative 0; Mismatches 97; Indels 0; Gaps 0;

QY 2054 CAATCTCTCCCTTGAATTGAAGTGAACATCACTTGAACAAAGTTCACCTGTCAT 2113
 DB 1 CGAATCTCTCCCTTGAATTGAATTGAACATCACTTGAACAAAGTTCACCTGTCAT 60

QY 2114 GGAACCCAGGCGATGACACAAATAGCCCATTAACAAATTCATCATCGAATATGAAGATG 2173
 DB 61 GGAACCCAGGCGATGACACAAATAGCCCATTAACAAATTCATCATCGAATATGAAGATG 120

QY 2174 CAATGACAAAGCCAGGCGTGTGGACCAACCAACTGAAGTTTGTGAAACAGACACAG 2233
 DB 121 CAATGACAAAGCCAGGCGTGTGGACCAACCAACTGAAGTTTGTGAAACAGACACAG 180

QY 2234 CCCAGCTGAAGTGTCTCTTACAGTGAACCTCTCTCCGGTGTATGGCACTGAACACCA 2293
 DB 181 CCCAAGCTGAAGTGTCTCTTACAGTGAACCTCTCTCCGGTGTATGGCACTGAACACCA 240

QY 2294 TTGGGAAGAGCTGTGCCAGCGAGCGTGTGACAGTATTTGACGAAAGCCTCAGAACAG 2353
 DB 241 TTGGGAAGAGTGTGCCAGCGAGCGATTCGACAGTATTTTCAAAAGCCGACAGACAG 300

QY 2354 ATAAAAACCCCAACAGCTGTGAAGGACGTGGATCGAAGCTGATATTTGAAGATTACGT 2413
 DB 301 ATCAAGATCCCATGCTGTGAAGGACGTGGATCGAAGCTGATATTTGAAGATTACGT 360

QY 2414 GGAACCCCTTGAATGTTTCCATTTATTTGGGCCAGGCTTCATGACAAAGTTGCTGGC 2473
 DB 361 GGAACCCCTTGAATGTTTCCATTTATTTGGGCCAGGCTTCATGACAAAGTTGCTGGC 420

QY 2474 GCCAAGAAATGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2533
 DB 421 GCCAAGAAATGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480

QY 2534 TTGTCTCAGGACCGCAACCTTTTGTTCATACCTGATCAAGTTCAGGCTCGAATGACA 2593
 DB 481 TTGTCTCAGGACCGCAACCTTTTGTTCATACCTGATCAAGTTCAGGCTCGAATGATG 540

QY 2594 TGGGGTTTGGCCCGGACGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2653
 DB 541 TGGGGTTTGGCCCGGACGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 600

QY 2654 TGGCTCTTGGGACGTGGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 2713
 DB 601 TGGCTCTTGGGACGTGGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 660

QY 2714 ACCCAGTACCTTGAAGAACATCCGAGGACCACTCAAGAGCTATTCATTTATTTGGA 2773
 DB 661 ACCCAGTACCTTGAAGAACATCCGAGGACCACTCAAGAGCTATTCATTTATTTGGA 720

QY 2774 AGACCCAGAGTTCATCTAAAGAAACAGACGTCACAT 2810
 DB 721 AGACCCAGAGTTCATCTAAAGAAACAGACGTCACAT 757

RESULT 10
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 LOCUS UI-M-FRO-cdz-1-15-0-UI.r1 NIH_BMAP_FRO Mus musculus cDNA clone
 CA327466
 DEFINITION IMAGE:6826552 5', mRNA sequence.
 CA327466
 ACCESSION CA327466.1 GI:24545564
 VERSION
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)

ORGANISM
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
 AUTHORS NIH-MGC http://img.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgaabs-remail.nih.gov
 Tissue Procurement: Dr. Jim Lin, University of Iowa
 cDNA library preparation: Dr. M. Bento Soares, University of Iowa
 DNA library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LMD at:
 http://imgc.nih.gov
 This clone was contributed by the Brain Molecular Anatomy Project (BMAP)
 Seq primer: pyx-5.

FEATURES
source

Location/Qualifiers
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/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:6826552"
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/dev_stage="embryo 13.5,14.5,16.5,17.5,18.5,19.5,20.5,21.5,22.5,23.5,24.5,25.5,26.5,27.5,28.5,29.5,30.5,31.5,32.5,33.5,34.5,35.5,36.5,37.5,38.5,39.5,40.5,41.5,42.5,43.5,44.5,45.5,46.5,47.5,48.5,49.5,50.5,51.5,52.5,53.5,54.5,55.5,56.5,57.5,58.5,59.5,60.5,61.5,62.5,63.5,64.5,65.5,66.5,67.5,68.5,69.5,70.5,71.5,72.5,73.5,74.5,75.5,76.5,77.5,78.5,79.5,80.5,81.5,82.5"
/lab_host="PH10B (T1 phage resistant)"
/clone_1ib="NIH BMAP F10"
/note="Organ: Brain; Vector: pYX-Asc; Site 1: Ecor I; Site 2: Not I; The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with Ecor I adaptor, digested with NotI and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is AGGAGACAG. This library was created for the University of Iowa Brain Anatomy Project (BMAP), supported by National Institute of Mental Health (NIMH), Hemm Chin, Ph.D., program coordinator."

ORIGIN

Query Match 14.5%; Score 601.4; DB 14; Length 824;
Best Local Similarity 87.1%; Pred. No. 7.7e-156;
Matches 659; Conservative 0; Mismatches 98; Indels 0; Gaps 0;

55 AATCTTTTGAAGAAAGAAAGAAATTCAGTGTGTGAGTCTCAGACAGAGTTAGCTA 114
115 ATGACGCTTAATAATATGCGGAAAGAGCGCTTATCGCGGAGAGCGCCCTGATT 174
127 ATGACGCTTAATAATATGCGGAAAGAGCGCTTATCGCGGAGAGCGCCCTGATT 186
175 CTCTTCCTGTGCAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 234
187 CTCTTCCTGTGCAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 246
235 GACTTGTGTGAG 294
247 GACTTGTGTGAG 306
295 CGGAGAAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 354
307 CGGAGAAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 366
355 ACCCGTAATGGAATCTTGTGATGATGATGATGATGATGATGATGATGATGATGAT 414
367 ACTCGTAATGGAATCTTGTGATGATGATGATGATGATGATGATGATGATGATGAT 426
415 AAGAGAAAG 474
427 AAGAGAAAG 486
475 TATCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 534
487 TATCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 546
535 CCATCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 594
547 CCATCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 606
595 CAGTCTTTTGAAG 654
607 CAGTCTTTTGAAG 666
655 ATGAGTAATTCCTTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 714

Db 667 ATGATTAATTCCTTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 726
715 GACCTTTTGAAG 774
727 GACCTTTTGAAG 786
775 AGATTTAATTCCTTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 811
787 AGATTTAATTCCTTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 823

RESULT 11
CF741342 752 bp mRNA linear EST 10-OCT-2003
LOCUS
DEFINITION
CF741342
IMAGE:30618401 5', mRNA sequence.

ACCESSION
CF741342
VERSION
CF741342.1 GI:37637680
KEYWORDS
EST.
SOURCE
Mus musculus (house mouse)

ORGANISM
Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
NIH-MGC http://mgi.nci.nih.gov/
1 (bases 1 to 752)
REFERENCE
Unpublished (1999)
CONTACT: Robert Strausberg, Ph.D.
Email: cga@bbs-rmail.nih.gov
Tissue Procurement: Dr. James Lin, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/mouse1.html
This clone was contributed by the Brain Molecular Anatomy Project (BMAP)

FEATURES
source

Location/Qualifiers
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/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:30618401"
/tissue_type="whole brain"
/dev_stage="1, 5, and 15 days newborn"
/lab_host="PH10B (T1 phage resistant)"
/clone_1ib="NIH BMAP GH0"
/note="Organ: Brain; Vector: pYX-Asc; Site 1: Ecor I; Site 2: Not I; The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with Ecor I adaptor, digested with NotI and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is CGAAGTAAT. This library was created for the University of Iowa Brain Anatomy Project (BMAP), supported by National Institute of Mental Health (NIMH), Hemm Chin, Ph.D., program coordinator."

ORIGIN

Query Match 14.5%; Score 598.8; DB 14; Length 752;
Best Local Similarity 87.9%; Pred. No. 3.9e-155;
Matches 662; Conservative 0; Mismatches 90; Indels 1; Gaps 1;
878 CTGAGTTTATGAGTCTAATCAAGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 937

Db 1 CTGAGTTTATGCTGCTAAATCTAGTAAAGAGAGGCC-CCAACTTTTCTTACTCCAGAGG 59

Qy 938 GGAATGCAAGTAAACAAAGGAATTAAGAGAAATGTGCTTCACTGAGAGCATGGCAG 997

Db 60 GCAATGAAGAACCAAGAGAGATTAAGAGAAACCTGCTTCCGCTGAGTCCATTGCGG 119

Qy 998 AAGGACATGCTCAATCCCAATTTATTTACTGGGCAAGAGAGATGGAATGCTACCCAAAACA 1057

Db 120 AAGGCTACTACTCTCCAAATTTATTTACTGATCAAGAGAAACGGAATGCTTCCCGCAACC 179

Qy 1058 GGAAGCTTTATTAAGAACTTTGAGAAAACCTTGCAGATCTTCACTGTTTCAAGAGCAGAT 1117

Db 180 GGAACATTTTATCGGAATTTAAGAAAACCTGCAAGATCACTAGTTTCCGAAGCGACT 239

Qy 1118 CTGGAATTTACCAATGATAGCAAAAATGACATTTAGAGCCATCCCATCATCTTCTG 1177

Db 240 CTGGAATTTATCGATGATAGCAAAAATGACATTTAGAGCCATCCCATCATCTTCTG 299

Qy 1178 TTAGAGTTAAAGGCTCCATCTGATGACAGCCCTGCAAAATCTTGTGCTGCCAG 1237

Db 300 TCACTGTTAAAGGCTCCCTCACTGATGATGAGCAGCTCAAAACCTGCTTCCCGG 359

Qy 1238 GAGAGATGAGACCTTGAATGTCAGAGCTAATGCAACCCCAACCAATTAAGTCTGT 1297

Db 360 GAGAGATGAGACCTTCACTGATGAGCTAATGCAACCCCAACCAATTAAGTCTGT 419

Qy 1298 TAAACAATGAGAGTCCCAATGAAATGAGCCCTGATGATGACCCCAAGAAATAGATGAGG 1357

Db 420 TAAACAATGAGAGTCCCAATGAAATGAGCTTCTGATGATGACCCCAAGAAATAGATGAGG 479

Qy 1358 ATACCATTTATTTTCAAAATGTTCAAGAAATGACATGATATATCATGATGATGCT 1417

Db 480 ATACCATTTATTTTCAAAATGTTCAAGAAATGACATGATGATATATCATGATGATGCT 539

Qy 1418 CTAAATGATGATGATTTTAACTGCAAGAGCATTTGTAATGCTGCTGAGCCACCCAG 1477

Db 540 CTAAATGATGATGATTTTAACTGCAAGAGCATTTGTAATGCTGCTGAGCCACCCAG 599

Qy 1478 GAATCTCACTGCACTGCAAGAGCATTTGTAATGCTGCTGAGCCACCCAG 1537

Db 600 GGAATCTCACTGCAAGAGCATTTGTAATGCTGCTGAGCCACCCAG 659

Qy 1538 ACTGTCCTTCTTGGGCTCTCTCCCAACCATGAGTGTAAAGAGCTAAAGAA 1597

Db 660 ATTGTCCTTCTTGGGCTCTCTCCCAACCATGAGTGTAAAGAGCTAAAGAA 719

Qy 1598 GTGCTCTTCAAGAGATTTTATGTTTATCATG 1630

Db 720 GCGCTCTTCAAGAGATTTTATGTTTATGATG 752

RESULT 12

AK052440

LOCUS AK052440 3037 bp mRNA linear HTC 20-SEP-2003

DEFINITION Mus musculus 13 days embryo lung cDNA, RIKEN full-length enriched library, clone: D430023G06 product: NEUROFASCIN (FRAGMENT) homolog [Rattus norvegicus], full insert sequence.

ACCESSION AK052440

VERSION AK052440.1 GI:26095186

KEYWORDS HTC; CAP trapper.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE 1 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 2 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Komno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.

TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes

JOURNAL Genome Res. 10 (10), 1617-1630 (2000)

MEDLINE 20499374

PUBMED 11042159

REFERENCE 3

AUTHORS Shibata, K., Itoh, M., Aizawa, K., Nagao, S., Sasaki, N., Carninci, P., Komno, H., Akiyama, J., Nishi, K., Kitahara, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kaishiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Matsubara, K., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kito, A. and Hayashizaki, Y.

TITLE RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer

JOURNAL Genome Res. 10 (11), 1757-1771 (2000)

MEDLINE 20530913

PUBMED 11076861

REFERENCE 4

AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.

TITLE Functional annotation of a full-length mouse cDNA collection

JOURNAL Nature 409, 685-690 (2001)

REFERENCE 5

AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

JOURNAL Nature 420, 563-573 (2002)

REFERENCE 6

AUTHORS Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagata, T., Hara, A., Hashizume, M., Hayashida, K., Hayatsu, N., Hiramoto, N., Hirooka, T., Hirozane, T., Hori, F., Imocani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Komno, H., Kouda, M., Koya, S., Kuribara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Nunazaki, R., Ohno, M., Ohsato, N., Sano, H., Sasaki, D., Shibata, K., Shingawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.

TITLE Direct Submission

JOURNAL Submitted (16-JUL-2001) Yoshinori Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration and Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan [E-mail: genome-res@gsr.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216]

COMMENT CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken contributed to prepare mouse cDNAs.

PLEASE VISIT OUR WEB SITE FOR FURTHER DETAILS.

URL: http://genome.gsc.riken.go.jp/

URL: http://fantom.gsc.riken.go.jp/

FEATURES

source location/Qualifiers

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/db_xref="taxon:10090"

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/dev_stage="13 days embryo"

1..3037

/note="NEUROFASCIN (FRAGMENT) homolog [Rattus norvegicus] (SPT8) p97685, evidence: FASTV, 95.9%ID, 67.6%length."

misc_feature

ORIGIN

match=2449)

Query Match 14.5%; Score 598.8; DB 11; Length 3037;
Best Local Similarity 54.0%; Pred. No. 7.9e-155;
Matches 1317; Conservative 0; Mismatches 1092; Indels 77; Gaps 4;

235 GACTTGATGAGAGCTTCAACCATCAACCAAGTCTCCAAAGATTATATTAAGCCCT 294
307 GACCTGACCCCAACCCCACTATCAACAGCAAGTCCGTAAGAGCAACATCGAGCCCT 366
295 GCGGAGATATTTGTAATCCAGTGTGAAGCCAAAGGAAACCGCCCAAGCTTTCTG 354
367 CGAGATTAACATCTGATTAATGTAAGTAAGGCAACCCGCCCCAGTTTCTACTG 426
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427 ACTCGAAGAGCATTTCTCAACATTCGCAAGACCCAGGCTGTCCATGAGAGAGAA 486
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487 TCTGGAGCTTGTGATGACATTCGCAATGTTGGGCGGCTGAGGAAATACGAGGGAG 546
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535 CCATCAAGTCAACATGTGAGCAAGAAAGAAATTTGAACCAATCACTTCAAGTGT 594
607 GTGTCAAAATCTCCCTGTGGCCCAAGAAACCTAGACCCGCTGTGTTCAGAGAGGT 666
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667 GCCCTTGTACACTACAGTGAACCCCAACCCGCTCTCCCTCCCTCACTTCTTGG 726
655 ATGATTAATCTCTTCAAGACTTCCCAAGTGAAGATTTCTCAAGTGTGAATGG 714
727 ATGACAGCTCATGAGGCCATCAACGAGCAAGCGTGTCTCCAGAGGTCAACAAGG 786
715 GACCTTATTTTCCCAATGCTCTCCAGAGGACCCCGGAAGCTATATCTGTATGCT 774
787 GACCTGTACTTCCCAAGCTCATGCTGACAGCAATGCAACCGACTACAGC--CAACGG 844
775 AGATTTAATCATACTCAACCATATACAGCAAGCAACCTATTTCTGTGAAGGATTTCA 834
845 CGCTTTCACCTTCAACCAACCAATTCAGCAAGAAACCCCTCAACCTCAAGGCTCTCAC 904
835 GTGATGAATTAATGACATTAATGCTGCTAATTTGAAGTGAACATGAGTTTATGCTGT 894
905 ACCGAGGAGT----- 915
895 AAATCAAGTAGAGAGAGGCCCAACATTTTAACTCCAGAAAGGCAATGCAATCAAA 954
916 -----TGCAAGAAAGAACGCCAGCTTCAATGATTCACAGGAGCAATCGAGCTGAG 967
955 GAGGAATTAAGAGAAATGCTTTCACATGAGTGTGAGGAGAGAGTGTGCTTCCCA 1014
968 ATGTTCTTCCGTGAGTGAAGCTGCTGTGATGATTTGCTTGTGAGCTTCCAAACACCA 1027
1015 ATTATTTACGTGGGCAAGAGAGATGATGCTTACCCAAACAGCAAGTATTAAGAAC 1074
1028 GACATTTGATGTGTACAAAGAAAGTGGGAGCTCCCATCTAACAGGCCAAGTTTCAGAAC 1087
1075 TTTGAGAAACCTTGTGAGATCAATGATTTTCAAGAGAGAGCTTGTGAATTAACAAATGT 1134
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1135 ATAGCAAAATATGATTAAGAGCATTCACATCACTTCTGTAGAGTTAAAGGAGGT 1194
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1195 CCATACGTGATCAAGCCCTTCAAAATCTTGTGTGTCTCCAGAGAGATGGGACCTTG 1254

1208 CCATACGTGATGAGAGCCCAAGAACTGATCTGTGCTCTGGGAGAGTGGAGGCTG 1267
1255 ATCTGAGAGTATATGAGCAACCCCAACCAAGATTTAGTGTGTTAAACAAATGAGTCCCA 1314
1268 GTATCCGAGACCAATGAGAACCCCAAGCCGACCGTGTGAGTGTGATGATGAGAGCTT 1327
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1328 TTACATGAGGACCAACCAATCCCAACCTGAGTGTGAGGACATATCATCTTCCGG 1387
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1495 AACACACTCAACAGATCAATGCAACAGGCTGTGTTACTAGACTGTGCTTCTTGG 1554
1508 AACAGCTCATGAGGATGATCTTTATACGAGCAACGAGCTGAGCTGTCTTGG 1567
1555 TCTCTCTCCCAACCATGAGTGTGTTAAGAGCTTAAAGAGTGTCTTCTTCAATGAT 1614
1568 TCTCCCATCCCAACCTCCGATGTTTAAAGATGGGCAAGAGCAACCTGATGCGGT 1627
1615 ATTTATGTTTATCATGAATAATGAACTTTGAATCAATGAATGATGATGATGATGAT 1674
1628 AACTACAGCTTACAGAAACGAGCTGTAGAAATCAAGATGATGATGATGATGATGATG 1687
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1795 AGCATGTGTCTTGTATGATGAATGAAATGAATGATCACTTATCCCTCACTGTCTG 1854
1808 ACCAGGTGAGCTGAGATGCTGCGGTGAACATGACCTCTTGAAGCTCAACATCTCC 1867
1855 TGGTGAAGAGCAACAGAGGAACTGCGCATGATGAAGATTTCACTGTGACAAAGATAT 1914
1868 TGGTGAAGAGAGATGAGCACTCTACATTTGAAGAAAGAGATGAAGAGATATCTCC 1927
1915 CTAGTGTAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1974
1928 CTGAGATCTTGTGAGTGGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1987
1975 ACTGTGACAGCTGTCCGCAAGGCTGTGTGATGCTGTGTGTGTGTGTGTGTGTGTGT 2034
1988 GAGCTGAGCAAGAGCTGGCAAGAGCTTACTCTGCTGTGTGTGTGTGTGTGTGTGTGT 2047
2035 GCTCCGTTTACGATGTC-----CCAAATCTCTCTTGTGATTAAGATG 2079
2048 ACTAACCTGTGTGCTGTGCTTACCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2107
2080 ACAAGTCACTTGAACAAAGTGTTCAGCTGTATGATGATGATGATGATGATGATGATGAT 2139
2108 ACTGACCTGTGTGAGAGAGTGTGATGATGATGATGATGATGATGATGATGATGATGAT 2167
2140 CCAATTAACAAATTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2199
2168 CCAATTAACAAATTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2227
2200 CACCAAACTGAAGTTTCTGAAACAGACCAAGCCAGCTGAGAGTGTCTCTTACGTC 2259
2228 GACCACTCAGATTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2287
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RESULT 14
 BX505499 594 bp mRNA linear EST 04-SRP-2003
 LOCUS DKFZp686i117202.r1.686 (synonym: hicc3) Homo sapiens cDNA clone
 DEFINITION DKFZp686i117202.5', mRNA sequence.
 ACCESSION BX505499
 VERSION BX505499.1 GI:32034972
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 594)
 Poustka, A., Albert, R., Moosmayer, P., Schupp, I., Wellenreuther, R.,
 Mewes, H.W., Well, B., Amid, C., Osanger, A., Fodor, G., Han, M. and
 Wiemann, S.
 TITLE EST (Poustka, A., Albert, R., Moosmayer, P., Schupp, I.,
 Wellenreuther, R., et al.)
 JOURNAL Unpublished (2003)
 COMMENT Contact: MIPS
 MIPS Ingolstaedter Landstr.1, D-85764 Neuberg, Germany
 This is the 5' sequence of the clone insert
 Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
 Research Center (DKFZ); Email: s.wiemann@dkfz-heidelberg.de;
 sequenced by DKFZ (German Cancer Research Center,
 Heidelberg/Germany) within the cDNA sequencing consortium of the
 German Genome Project.
 No si sequence available.
 This clone (DKFZp686i117202) is available at the RZPD in Berlin.
 Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
 FEATURES
 source
 1..594
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="DKFZp686i117202"
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 /note="Vector: pTriblX2; Site_1: SfiI; Site_2: SfiI;
 cDNA-collection"

ORIGIN
 Query Match 13.4%; Score 553; DB 13; Length 594;
 Best Local Similarity 100.0%; Pred. No. 2.1e-142;
 Matches 553; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2749 CAAGCTATCGGATTCTATTGGAAGACCGAGTCTCTTAAAGAAACAGAGCTC 2808
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 DB 1 CAAGCTATCGGATTCTATTGGAAGACCGAGTCTCTTAAAGAAACAGAGCTC 60
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 QY 2809 ATTGAGAAAAAATCTCTCACTTCCAGGACCAAGACTCATGTGCGGGGCTA 2868
 |||||
 DB 61 ATTGAGAAAAAATCTCTCACTTCCAGGACCAAGACTCATGTGCGGGGCTA 120
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 QY 2869 GAGCCCTTTAGCCACTACACACTGATGTCCAGTGTGCAATGGAGGAGGAGGCCA 2928
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 DB 121 GAGCCCTTTAGCCACTACACACTGATGTCCAGTGTGCAATGGAGGAGGAGGCCA 180
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 QY 2929 GCGAGCCCTGAGAGAGCTCTTAATACTCGAAGAGAGTCCCAAGTCTCCCTGCTTTG 2988
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 DB 191 GCGAGCCCTGAGAGAGCTCTTAATACTCGAAGAGAGTCCCAAGTCTCCCTGCTTTG 240
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 QY 3049 AATGCAATTTTGAACAGAGTACCTTAAAGATACAGCCAAATTACAGCACACATGAATTA 3108
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QY 3109 GGCCTCTGTAGATTGTAATAATTCCTGCACAAGACAGGTGACCTTAAAAAATTTA 3168
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 QY 3229 CAATTACAGAGAGACGCTACCACTGTGATGAAGCTGTATCTTCCACTATGTA 3288
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 DB 481 CAATTACAGAGAGAGACGCTACCACTGTGATGAAGCTGTATCTTCCACTATGTA 540
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 QY 3289 GGTGACGCAAG 3301
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 DB 541 GGTGACGCAAG 553
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RESULT 15
 CD804797 775 bp mRNA linear EST 15-JUL-2003
 LOCUS CD804797
 DEFINITION UI-M-GMO-cig-m-20-0-UI.r1 NIH_BMAP_GMO Mus musculus cDNA clone
 IMAGE:30538963 5', mRNA sequence.
 ACCESSION CD804797
 VERSION CD804797.1 GI:32463623
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 775)
 NIH-MGC <http://mgc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Dr. Jim Lin, University of Iowa
 cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Distribution information can be found at
<http://genome.uiowa.edu/distribution/mouse1.html>
 This clone was contributed by the Brain Molecular Anatomy Project
 (BMAP)
 Seq primer: PYX-5.
 Location/Qualifiers
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 /mol_type="mRNA"
 /strain="CS7BL/6"
 /db_xref="taxon:10090"
 /clone="IMAGE:30538963"
 /tissue_type="whole eye"
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 /lab_host="NIH BMAP GW0"
 /note="Organ: Eye; Vector: PYX-Acc; Site 1: EcoR I;
 Site 2: Not I; The library was constructed according
 to Bonaldi, Lennon and Soares, Genome Research, 6:791-806,
 1996. Denatured RNA was size fractionated on a 1% agarose
 gel. First strand cDNA synthesis was primed with oligo-dT
 primer containing a Not I site. Double strand cDNA was
 size selected according to mRNA size fraction, ligated
 with EcoR I adaptor, digested with NotI and then cloned
 directionally into PYX-Acc vector. The library tag
 sequence located between the Not I site and the polyA tail
 is CTGGCTCTC. This library was created for the University
 of Iowa Brain Anatomy Project (BMAP). 'Gene Discovery in the
 Developing Mouse Nervous System', supported by National
 Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
 program coordinator."

FEATURES
 source
 1..775
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="CS7BL/6"
 /db_xref="taxon:10090"
 /clone="IMAGE:30538963"
 /tissue_type="whole eye"
 /dev_stage="embryo 15.5, 16.5, 17.5, 18.5 dpc"
 /lab_host="NIH BMAP GW0"
 /note="Organ: Eye; Vector: PYX-Acc; Site 1: EcoR I;
 Site 2: Not I; The library was constructed according
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 with EcoR I adaptor, digested with NotI and then cloned
 directionally into PYX-Acc vector. The library tag
 sequence located between the Not I site and the polyA tail
 is CTGGCTCTC. This library was created for the University
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 Developing Mouse Nervous System', supported by National
 Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
 program coordinator."

ORIGIN

